

CTG GYN GCT GGT TAT GCT CAT GAT GAT GAC TGG ATT GAC CCC ACA GAC	219
Leu Xaa Ala Gly Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp	
-5 1 5 10	
ATG CTT AAC TAT GAT GCT GCT TCA GGA ACA ATG AGA AAA TCT CAG GCA	267
Met Leu Asn Tyr Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala	
15 20 25	
AAA TAT GGT ATT TCA GGG GAA AAG GAT GTC AGT CCT GAC TTG TCA TGT	315
Lys Tyr Gly Ile Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys	
30 35 40	
GCT GRT GAA ATA TCA GAA	333
Ala Xaa Glu Ile Ser Glu	
45	

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 129..278
id R18809
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 71..129
id R18809
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 299..347
id R18809
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..441
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 141..277
id R88070
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..300
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..134
id R88070
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 68..217
id T85919
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 98..157
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 9..68
id T85919
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..317
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 129..288
id R60434
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 99..157
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 71..129
id R60434
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 86..235
id W23910
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 27..86
id W23910
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 325..381
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LVXSLPVHCLTFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

AAGTTGGTGG AGTTCTGCCC GGATGGAAGC TCCGGCCGCG GAGTGATGGT GGCCTCAGCG      60
AAGATGGGCC GGGCAGGGAC CATGGCGGTG GCAGCAGAGC TTCGAGAGCT GTGCCCAGGA      120
GTGAACAACC AGCCCTACCT CTGTGAGAGT KGTCACCTGC TCGGGGAAM CTGGCTGCTG      180
CACCTACTAC TATGAGCTCT GGTGGTTCTG GCTGCTCTGG ACTGTCCTCA TCCTCTTTAG      240
CTGCTGTTGC GCCTCCGCC ACCGACGAGC TAAACTCAGG CTGCAACAAC AGCAGCGGCA      300
SSTGAAACAA CTTGTTGGCC TATC ATG GGG CAT GCC ATG GGG CTG GTN STT      351
                Met Gly His Ala Met Gly Leu Val Xaa
                -15

TCC CTA CCG GTT CAC TGC TTG ACC TTC GCT TCC TCA GCA CCT TCA AGC      399
Ser Leu Pro Val His Cys Leu Thr Phe Ala Ser Ser Ala Pro Ser Ser
-10                -5                1                5

CCC CAG CCT ACG AGG ATG TGG TTC AMC GCC CAG GCA CAC CAM CCC CCC      447
Pro Gln Pro Thr Arg Met Trp Phe Xaa Ala Gln Ala His Xaa Pro Pro
                10                15                20

CTT ATA CTG GGC CCG      462
Leu Ile Leu Gly Pro
                25

```

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 156..288
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..133
id AA081350
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 289..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 133..240
id AA081350
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 422..453
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 269..300
id AA081350
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 289..453
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 67..231
id AA046671
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..289
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..68
id AA046671
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 104..151
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWTR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AATAGTTCCA GAACTCTCCA TCCGGACTAG TTATTGAGCA TCTGCCTCTC ATATCACCAG 60

TGGCCATCTG AGGTGTTTCC CTGGCTCTGA AGGGGTAGGC ACG ATG GCC AGG TGC 115
Met Ala Arg Cys

-15

TTC AGC CTG GTG TTG CTT CTC ACT TCC ATC TGG ACC ACG AGG CTC CTG	163
Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr Thr Arg Leu Leu	
-10 -5 1	
GTC CAA GGC TCT TTG CGT GCA GAA GAG CTT TCC ATC CAG GTG TCA TGC	211
Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile Gln Val Ser Cys	
5 10 15 20	
AGA ATT ATG GGG ATC ACC CTT GTG AGC AAA AAG GCG AAC CAG CAG CTG	259
Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala Asn Gln Gln Leu	
25 30 35	
AAT TTC ACA GAA GCT AAG GAG GCC TGT AGG CTG CTG GGA CTA AGT TTG	307
Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu Gly Leu Ser Leu	
40 45 50	
GCC GGC AAG GAC CAA GTT GAA ACA GCC TTG AAA GCT AGC TTT GAA ACT	355
Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala Ser Phe Glu Thr	
55 60 65	
TGC AGC TAT GGC TGG GTT GGA GAT GGA TTC GTG GTC ATC TCT AGG ATT	403
Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val Ile Ser Arg Ile	
70 75 80	
AGC CCA AAC CCC AAG TGT GGG AAA AAT GGG GTG GGT GTC CTG ATT TGG	451
Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly Val Leu Ile Trp	
85 90 95 100	

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 67..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..301
id AA056199
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..215

id R66275
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..221
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 99..203
id AA054476
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..120
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 22..103
id AA054476
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 232..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..135
id AA143025
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 242..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 84..208
id W90481
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 175..351
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq VLAQLAFLSQISQ/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```
ACTTTTCCGG CTGACTTCTG AGAAGGTTGC GCASAGCTGT GCCCGGCAGT CTAGAGGCGC   60
AGAAGAGGAA GCCATCGCCT GGCCCCGGCT CTCTGGACCT TGTCTCGCTC GGGAGCGGAA  120
ACAGCGGCAG CCAGAGAACT GTTTTAATCA TGGACAAACA AAACTCACAG ATGA ATG      177
                                         Met
CTT CTC ACC CGG AAA CAA ACT TGC CAG TTG GGT ATC CTC CTC AGT ATC      225
Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser Ile
-55                               -40                               -45
CAC CCA CAG CAT TCC AAG GAC CTC CAG GAT ATA GTG GCT ACC CTG GGC      273
```

His	Arg	Gln	His	Ser	Lys	Asp	Leu	Gln	Asp	Ile	Val	Ala	Thr	Leu	Gly		
	-40						-35					-30					
CCC	AGG	TCA	GCT	ACC	CAC	CCC	CAC	CAG	CCG	GCC	ATT	CAG	GTC	CTG	GCC	321	
Pro	Arg	Ser	Ala	Thr	His	Pro	His	Gln	Pro	Ala	Ile	Gln	Val	Leu	Ala		
	-25					-20				-15							
CAG	CTG	GCT	TTC	CTG	TCC	CAA	ATC	AGC	CAG	TGT	ATA	ATC	AGC	CAG	CGG	369	
Gln	Leu	Ala	Phe	Leu	Ser	Gln	Ile	Ser	Gln	Cys	Ile	Ile	Ser	Gln	Arg		
-10					-5					1				5			

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 211..339
id AA284366
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 166..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 92..226
id AA284366
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 72..177
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..106
id AA284366
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 199..282
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

AGAACATAGG TTGCCTTAGA GAGGTTCCCC GGTGTCCCGA CGGCGGCTCA AGTCAGAGTT    60
GCTGGGTTTT GCTCAGATTG GTGTGGGAAG AGCCTGCCTG TGGGGAGCGG CCACTCCATA    120
CTGCTGARGC CTCAGGACTG CTGCTCAGCT TGCCCGTTAC CTGAAGAGGC GGCGGAGCGG    180
NGCCCCTGAC CGGTCACC ATG TGG GCC TTC TCG GAA TTG CCC ATG CCG CTG    231
                Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu
                        -25                      -20

CTG ATC AAT TTG ATC GTC TCG CTG CTG GGA TTT GTG GCC ACA GTC ACC    279
Leu Ile Asn Leu Ile Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr
        -15                      -10                      -5

CTC ATC CCG GCC TTC CGG GGC CAC TTC ATT GCT GCG CGC CTC TGT GGT    327
Leu Ile Pro Ala Phe Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly
        1                      5                      10                      15

CAG GAC CTC AAC AAA ACC AGC CGA CAG CAG ATC CCA GAA TCC CAG GGA    375
Gln Asp Leu Asn Lys Thr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly
                20                      25                      30

GTG ATC AGC GGT GCT GTT TTC CTT ATC ATC CTC TTC TGC
Val Ile Ser Gly Ala Val Phe Leu Ile Ile Leu Phe Cys    414
        35                      40

```

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 209..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 241..373
id H87867
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 63..159
id H87867

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..207
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 201..240
id H87867
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 224..459
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..236
id N87591
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..453
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 65..255
id AA172091
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 202..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 4..53
id AA172091
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..459
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 38..234
id H85080
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 225..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..37
id H85080
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 212..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4

seq PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

GACGCGCTGC GGCTCAGCGA CGCGGCTTCT AGAACCGGGT GATTGAACTA AACCTTCGCC      60
GCACCGAGTT TGCAGTACGG CCGTCACCCG CACCGCTGCC TGCTTGCGGT TGGAGAAATC      120
AARGGGCCCT ACCGGGCCTC CGTAGTCACC TCTCTATAGT GGGCGTGGCC GAGGCCGGGG      180
TGACCCTGCC GGAGCCTCCG CTGCCAGCGA C ATG TTC AAG GTA ATT CAG AGG      232
                               Met Phe Lys Val Ile Gln Arg
                               -20

TCC GTG GGG CCA GCC AGC CTG AGC TTG CTC ACC TTC AAA GTC TAT GCA      280
Ser Val Gly Pro Ala Ser Leu Ser Leu Leu Thr Phe Lys Val Tyr Ala
-15                               -10                               -5

GCA CCA AAA AAG GAC TCA CCT CCC AAA AAT TCC GTG AAG GTT GAT GAG      328
Ala Pro Lys Lys Asp Ser Pro Pro Lys Asn Ser Val Lys Val Asp Glu
 1                               5                               10                               15

CTT TCA CTC TAC TCA GTT CCT GAG GGT CAA TCG AAG TAT GTG GAG GAG      376
Leu Ser Leu Tyr Ser Val Pro Glu Gly Gln Ser Lys Tyr Val Glu Glu
                20                25                30

GCA AGG AGC CAG CTT GAA GAA AGC ATC TCA CAG CTC CGA CAC TAT TGC      424
Ala Arg Ser Gln Leu Glu Glu Ser Ile Ser Gln Leu Arg His Tyr Cys
                35                40                45

GAG CCA TAC ACA ACC TGG TGT CAG GAA ACG TAC      457
Glu Pro Tyr Thr Thr Trp Cys Gln Glu Thr Tyr
 50                55

```

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 38..251
id T94226
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 225..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..149
id W95280
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 148..214
id W95280
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 2..124
id N55978
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 262..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 98..162
id N55978
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 379..437
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 270..328
id N55978
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 317..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 154..210
id N55978
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 20..427
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

AACCGTGGCC TCGGACGAA ATG GCG AAA AGT CTT TTG AAG ACA GCC TCT CTG      52
      Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu
      -135                               -130

TCT GGA AGG ACA AAA TTG CTA CAT CAA ACA GGA TTG TCA CTT TAT AGT      100
Ser Gly Arg Thr Lys Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser
-125                               -120                               -115                               -110

ACA TCC CAT GGA TTT TAT GAG GAA GAA GTG AAA AAA ACA CTT CAG CAG      148
Thr Ser His Gly Phe Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln
      -105                               -100                               -95

TTT CCT GGT GGA TCC ATT GAC CTT CAG AAG GAA GAC AAT GGC ATT GGC      196
Phe Pro Gly Gly Ser Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly
      -90                               -85                               -80

ATT CTT ACT CTG AAC AAT CCA AGT AGA ATG AAT GCC TTT TCA GGT GTT      244
Ile Leu Thr Leu Asn Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val
      -75                               -70                               -65

ATG ATG CTA CAA CTT CTG GAA AAA GTA ATT GAA TTG GAA AAT TGG ACA      292
Met Met Leu Gln Leu Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr
      -60                               -55                               -50

GAG GGG AAA GGC CTC ATT GTC CGT GGG GCA AAA AAT ACT TTC TCT TCA      340
Glu Gly Lys Gly Leu Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser
-45                               -40                               -35                               -30

GGA TCT GAT CTG AAT GCT GTG AAA TCA CTA GGA CTC CAG AGA CTT CCT      388
Gly Ser Asp Leu Asn Ala Val Lys Ser Leu Gly Leu Gln Arg Leu Pro
      -25                               -20                               -15

TTA ATA AGT GTT GCG CTG GTT CAA GGT TGG GCA TTG GGT GGA GGA GCA      436
Leu Ile Ser Val Ala Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala
      -10                               -5                               1

GCG
Ala
839

```

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..212

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 125..221
id HUMEST2D1
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 214..322
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 9..117
id AA115085
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 132..263
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq PLLKILHAAGAQG/EM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```
AATTTCAVVA TGCTGCCGAG GCCCTAGGAT CTGTGACTGC CACCCCTCCC CCCACCCGGG      60
CTCGGCGGGG GAGCGACTCA TGGAGCTGCC GTAAGTTTTA CCAACAGACT GCAGTTTCTT      120
TCACTACCAA A ATG ACA TCA TTT TCC ACC TCT GCT CAG TGT TCA ACA TCT      170
           Met Thr Ser Phe Ser Thr Ser Ala Gln Cys Ser Thr Ser
                   -40                               -35

GAC AGT GCT TGC AGG ATC TCT CCT GGA CAA ATC AAT SVG GTA CGA CCA      218
Asp Ser Ala Cys Arg Ile Ser Pro Gly Gln Ile Asn Xaa Val Arg Pro
   -30                -25                               -20

AAA CTG CCG CTT TTG AAG ATT TTG CAT GCA GCA GGT GCG CAA GGT GAA      266
Lys Leu Pro Leu Leu Lys Ile Leu His Ala Ala Gly Ala Gln Gly Glu
   -15                -10                               -5                               1

ATG TTC ACT GTT AAA GAG GTC ATG CAC TAT TTA GGT CAG TAC ATA ATG      314
Met Phe Thr Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met
           5                10                15

GTG AAG CAG      323
Val Lys Gln
      20
```

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 478 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 104..370
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..267
id AA114062
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 409..451
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 309..351
id AA114062
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 388..420
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 287..319
id AA114062
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 5..340
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.1
seq AFAWLGVVPLTAC/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

AAAG ATG GAC ACC GCG GAG GAA GAC ATA TGT AGA GTG TGT CGG TCA GAA	49
Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu	
-110 -105 -100	
GGA ACA CCT GAG AAA CCG CTT TAT CAT CCT TGT GTA TGT ACT GGC AGT	97
Gly Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser	
-95 -90 -85	
ATT AAG TTN GTC CAT CAA GAA TGC TTA GTT CAA TGG CTG AAA CAC AGT	145
Ile Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser	
-80 -75 -70	
CGA AAA GAA TAC TGT GAA TTA TGC AAG CAC AGA TTT GCT TTT ACA CCA	193
Arg Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro	
-65 -60 -55 -50	
ATT TAT TCT CCA GAT ATG CCT TCA CGG CTT CCA ATT CAA GAC ATA TTT	241
Ile Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe	
-45 -40 -35	

GCT GGA CTG GTT ACA AGT ATT GGC ACT GCA ATA CGA TAT TGG TTT CAT	289
Ala Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His	
-30 -25 -20	
TAT ACA CTT GTG GCC TTT GCA TGG TTG GGA GTT GTT CCT CTT ACA GCA	337
Tyr Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala	
-15 -10 -5	
TGC CGC ATC TAC AAG TGC TTG TTT ACT GGC TCC GTG AGC TCA CTA CTG	385
Cys Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu	
1 5 10 15	
ACG CTG CCA TTA GAT ATG CTG TCA ACG GAA AAT TTG TTG GCA GAT TGT	433
Thr Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys	
20 25 30	
TTG CAG GGT TGT TTT GTG GTG ACG TGC ACA CTG TGT GCA TTC ATC	478
Leu Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile	
35 40 45	

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 87..227
id W31692
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..121
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..77
id W31692
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 123..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 76..226
id H46855

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..76
id H46855
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 85..225
id H49687
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..121
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..75
id H49687
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 84..224
id H50194
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..121
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..75
id H50194
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 82..222
id AA285085
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..73
id AA285085
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 153..191
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq MLIMLGIFNVHS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```
CCCTGCGAGG GCATCCTGGG CTTTCTCCCA CCGCTTTCCTG AGCCCGCTTG CACCTCGGCG    60
ATCCCCGACT CCCTTCTTTA TGGCGTCGCT CCTGTGCTGT GGGCCGAAGC TGGCCGCCTG   120
CGGCATCGTG YRTCAGCGCC TGGGGAGTGA TC ATG TTG ATA ATG CTC GGA ATA     173
                               Met Leu Ile Met Leu Gly Ile
                               -10
TTT TTC AAT GTC CAT TCC GCT GTG TTG ATT GAG GAC GTT CCC TTC ACG     221
Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr
   -5              1              5              10
GAG AAA GAT TTT GAG ANT GGC CCC CAG AAC ATA TAC AAC CTT TAC GAG     269
Glu Lys Asp Phe Glu Xaa Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu
          15              20              25
CAT GGG                                           275
His Gly
```

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 82..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..142
id W24852
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 231..320

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 150..239
 id W24852
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 256..321
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 1..66
 id AA129007
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 321..350
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 65..94
 id AA129007
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 9..344
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.5
 seq AAVAVGMLXASYA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

AGAGGGTT ATG GGA GGG CTC TGG CGT CCT GGA TGG AGG TGC GTT CCT TTC	50
Met Gly Gly Leu Trp Arg Pro Gly Trp Arg Cys Val Pro Phe	
-110 -105 -100	
TGT GGC TGG CGC TGG ATC CAC CCT GGG TCT CCA ACC AGG GCT GCA GAG	98
Cys Gly Trp Arg Trp Ile His Pro Gly Ser Pro Thr Arg Ala Ala Glu	
-95 -90 -85	
AGG GTA GAG CCG TTT CTT AGG CCA GAG TGG AGT GGG ACA GGA GGT GCC	146
Arg Val Glu Pro Phe Leu Arg Pro Glu Trp Ser Gly Thr Gly Gly Ala	
-80 -75 -70	
GAG AGA GGA CTG AGG TGG CTT GGG ACA TGG AAG CGC TGC AGC CTT CGA	194
Glu Arg Gly Leu Arg Trp Leu Gly Thr Trp Lys Arg Cys Ser Leu Arg	
-65 -60 -55	
GCC CGG CAT CCA GCA TTG CAG CCG CCG CGG CGG CCT AAG AGC TCG AAC	242
Ala Arg His Pro Ala Leu Gln Pro Pro Arg Arg Pro Lys Ser Ser Asn	
-50 -45 -40 -35	
CCT TTC ACA CGC GCG SKV GAG GAG GAR CGG CGG CGG MAG AAC AAG ACG	290
Pro Phe Thr Arg Ala Xaa Glu Glu Glu Arg Arg Arg Xaa Asn Lys Thr	
-30 -25 -20	
ACC CTC ACT TAC GTG GCC GCT GTC GCC GTG GGC ATG CTN NGG GCG TCC	338
Thr Leu Thr Tyr Val Ala Ala Val Ala Val Gly Met Leu Xaa Ala Ser	
-15 -10 -5	

TAC GCT GCC GTA
Tyr Ala Ala Val
1

350

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..186
id W32758
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 132..248
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SDPLCVLFLNTSG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```
AAATCCCTGC GGTCCCAGCG TCGCTCCGGA CGCTGCCAAC CTGTTCTCCA CCGTCGCTCG      60
ACTTCCACCT CTAAGACTCC CACGAAACTC AGGTTGAATA ATTCAFCAA TTACACAAC      120
GAACTCAAGA C ATG GCT GCC CAG TGT GTC ACA AAG GTG GCG CTG AAT GTT      170
          Met Ala Ala Gln Cys Val Thr Lys Val Ala Leu Asn Val
          -35                                -30

TCC TGT GCC AAT CTT TTG GAT AAA GAT ATA GGG TCA AAG TCA GAC CCT      218
Ser Cys Ala Asn Leu Leu Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro
-25                                -20                                -15

TTA TGT GTG TTA TTT TTG AAT ACA AGT GGT CAA CAG TGG TAT GAG GTT      266
Leu Cys Val Leu Phe Leu Asn Thr Ser Gly Gln Gln Trp Tyr Glu Val
-10                                -5                                1                                5

GAG CGC ACA GAA AGG ATT AAG AAT TGC TTG AAT CCC CAA TTT TCC AAG      314
Glu Arg Thr Glu Arg Ile Lys Asn Cys Leu Asn Pro Gln Phe Ser Lys
          10                                15                                20
```

ACA TTT ATT ATT GAT TAC TAC TTT GAA GTG GTT CAG AAA TTG AAA TTT	362
Thr Phe Ile Ile Asp Tyr Tyr Phe Glu Val Val Gln Lys Leu Lys Phe	
25 30 35	
GGG GTT TAT GAC ATC GRC AAC AAA ACT ATT GAG CTG AGT GAT GAT GAC	410
Gly Val Tyr Asp Ile Xaa Asn Lys Thr Ile Glu Leu Ser Asp Asp Asp	
40 45 50	
TTC TTA GGG	419
Phe Leu Gly	
55	

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 35..374
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..301
id H81957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 373..404
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 298..329
id H81957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 2..316
id H62624
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 85..294
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPHTA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

AAGTGTCTCTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA GTAGTGGAAA      60
CGTTGCTTCTT GAGGGGAGCC CAAG ATG ACC GGT TCT AAC GAG TTC AAG CTG      111
           Met Thr Gly Ser Asn Glu Phe Lys Leu
           -70                               -65

AAC CAG CCA CCC GAG GAT GGC ATC TCC TCC GTG AAG TTC AGC CCC AAC      159
Asn Gln Pro Pro Glu Asp Gly Ile Ser Ser Val Lys Phe Ser Pro Asn
-60                               -55                               -50

ACC TCC CAG TTC CTG CTT GTC TCC TCC TGG GAC ACG TCC GTG CGT CTC      207
Thr Ser Gln Phe Leu Leu Val Ser Ser Trp Asp Thr Ser Val Arg Leu
-45                               -40                               -35                               -30

TAC GAT GTG CCG GCC AAC TCC ATG CGG CTC AAG TAC CAG CAC ACC GGC      255
Tyr Asp Val Pro Ala Asn Ser Met Arg Leu Lys Tyr Gln His Thr Gly
-25                               -20                               -15

GCC GTC CTG GAC TGC GCC TTC TAC GAT CCA ACG CAT GCC TGG AGT GGA      303
Ala Val Leu Asp Cys Ala Phe Tyr Asp Pro Thr His Ala Trp Ser Gly
-10                               -5                               1

GGA CTA GAT CAT CMV KTG AAA ATG CAT GAT TTG AAC ACT GAT CAA GAA      351
Gly Leu Asp His Xaa Xaa Lys Met His Asp Leu Asn Thr Asp Gln Glu
5                               10                               15

AAT CTT GTT GGG ACC CAT GAT GCC CCT ATC AGA TGT GTT GAA TAC TGT      399
Asn Leu Val Gly Thr His Asp Ala Pro Ile Arg Cys Val Glu Tyr Cys
20                               25                               30                               35

CCA AGT
Pro Ser
405

```

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 48..365
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..318
 id N31699
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 365..420
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 319..374
 id N31699
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 299..373
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.6
 seq AHLWCWCGSHCCST/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

AGTGTCCCT CAAATGGCGG TGTGAAGAGA GTTCGCCTGA GCCAGATCCC AGGTTTCACT   60
GAAGAACTT CTTAGAGATT CATTGCACTT CTGAGATTTA ATGTTTACAA CTTGGAGTTG  120
TCGACCTTCT TATAAGATAC ATTTTGAAG TCAAATGAA AGTTTCTGT GAAGTTTtag  180
AAGAGTTATA CAAGAAGGTA CTTCTGGAG CCACACTTGA AAATGACAGC CATGATTACG  240
TCTTTTATCT CAACCCAGCA GTTTCAGATC AAGATTGTTT TACAGCCACC TCCTTAGA   298
ATG GGC AAA CAC CTG TGG TAT CCA GGG CAG GCA TCA GCC CAT CTC TGT   346
Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys
-25          -20          -15          -10

TGG TGT GGC TCC CAT TGC TGT AGC ACC TGT GTG TTT GAA GAC CAA CTC   394
Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu
          -5              1              5

TCA GAT GAG CGG TTC CAG AGA AGT AAT GCT CCT TCA GTT AAC AGT GAT   442
Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp
      10              15              20

```

(2) INFORMATION FOR SEQ ID NO: 112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 81..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 3..308
id T23663
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 81..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 3..308
id T23653
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..297
id T03538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..217
id H28147
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 356..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 233..263
id H28147
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 144..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..225
id R71352
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 173..211
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq MLAVSLTVXLLGA/MM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

```

AGTGAGGTGG TTTCTGCGGG TGAGGCTGGC GCCCGTACCA TGAGCGAGGC GGACGGGCTG   60
CGACAGCGCC GGGCCCTGCG GCCCGCAAGT CGTCACAGAC GATGATGGCC AGGCCCCGGA  120
GGCTAAGGAC GGCAGCTCCT TTAGCGGCAG AGTTTTCCGA GTGACCTTCT TG ATG CTG  178
                                     Met Leu
GCT GTT TCT CTC ACC GTT CBC CTG CTT GGA GCC ATG ATG CTG CTG GAA   226
Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu Leu Glu
  -10                               -5                               1                               5
TCT CCT ATA GAT CCA CAG CCT CTC AGC TTC AAA GAA CCC CCG CTC TTG   274
Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro Leu Leu
          10                               15                               20
CTT GGT GTT CTG CAT CCA AAT ACG AAG CTG CGA CAG GCA GAA AGG CTG   322
Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu Arg Leu
          25                               30                               35
TTT GAA AAT CAA CTT GTT GGA CCG GAG TCC ATA GCA CAT ATT GGG GAT   370
Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile Gly Asp
          40                               45                               50
GTG ATG TTT ACT GGG AGC TGG                                       391
Val Met Phe Thr Gly Ser Trp
          55                               60

```

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..203
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..128
id R57344

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 128..159
id R57344
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 82..309
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq MLELDLLVFHLWG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```
AAGTAGCGCC TGCWGGCGGY GGCAGTTTGC CCGCGGRWGT GTGAAGGGAG ACAGTGTGGA      60
GGCCACAGGG TACTCGCCAC G ATG AGC AGC ACC TTA GCT AAG ATC GCG GAG      111
                               Met Ser Ser Thr Leu Ala Lys Ile Ala Glu
                               -75                               -70

ATA GAA GCA GAG ATG GCT CGG ACT CAA AAG AAC AAG GCC ACA GCA CAC      159
Ile Glu Ala Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Ala His
-65                               -60                               -55

CAC TTA GGG CTG CTT AAG GCT CGT CTT GCT AAG CTT CGT CGA GAA CTC      207
His Leu Gly Leu Leu Lys Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu
-50                               -45                               -40                               -35

ATT ACT CCA AAG GGT GGT GGT GGT GGA GGT CCA GGA GAA GGT TTT GAT      255
Ile Thr Pro Lys Gly Gly Gly Gly Gly Gly Pro Gly Glu Gly Phe Asp
-30                               -25                               -20

TGG CCA AGA CAG GTG ATG CTC GAA TTG GAT TTG TTG GTT TTC CAT CTG      303
Trp Pro Arg Gln Val Met Leu Glu Leu Asp Leu Leu Val Phe His Leu
-15                               -10                               -5

TGG GGA AGT CAA CAC TGC TTA GTA ACC TGG CAA GGG                        339
Trp Gly Ser Gln His Cys Leu Val Thr Trp Gln Gly
      1                               5                               10
```

(2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..198
id C18087
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..89
id T73970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 128..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 76..162
id T73970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 44..91
id T73946
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..142
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 13..95
id AA096472
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 144..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 96..125
id AA096472
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..214
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..46
id AA280423
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 47..181
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 13.9
seq LVLALLLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```
ATGGCGTAGA GCCTAGCAAC AGCGCAGGCT CCCAGCCGAG TCCGTT ATG GCC GCT      55
                                   Met Ala Ala
                                   -45

GCC GTC CCG AAG AGG ATG AGG GGG CCA GCA CAA GCG AAA CTG CTG CCC      103
Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys Leu Leu Pro
   -40                      -35                      -30

GGG TCG GCC ATC CAA GCC CTT GTG GGG TTG GCG CGG CCG CTG GTC TTG      151
Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro Leu Val Leu
   -25                      -20                      -15

GCG CTC CTG CTT GTG TCC GCC GCT CTA TCC AGT GTT GTA TCA CGG ACT      199
Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val Ser Arg Thr
  -10                      -5                      1                      5

GAT TCA CCG AGC CCA CTG      217
Asp Ser Pro Ser Pro Leu
   10
```

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 147..264
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 152..269
id AA015703
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 316..366
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 322..372
 id AA015703
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 257..302
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 261..306
 id AA015703
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 184..258
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 13.9
 seq LLSLLFLVQGAHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

AACAAAGAGT TGGCAGATCA CGGATGGAGG GCAGCATCTC CCAACAGCCT GGGCGGCCGC   60
TGAGACCCAG AGAACCCAAG GACTCCCCTK GGGGGYWCA Y CCAGCAGCCT CTGCTTCCCA  120
GGAGAGAGGT GCTGAAGTCC ACGAAGAGGT GGTGACTTCC AAGAGTGACT CCGTCGGAGG  180
AAA ATG ACT CCC CAG TCG CTG CTG CAG ACG ACA CTG TTC CTG CTG AGT   228
  Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser
   -25                      -20                      -15

CTG CTC TTC CTG GTC CAA GGT GCC CAC GGC AGG GGC CAC AGG GAA GAC   276
Leu Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp
 -10                      -5                      1                      5

TTT CGC TTC TGC AGC CAG CGG AAC CAG ACA CAC AGG AGC AGC CTC CAC   324
Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His
    10                      15                      20

TAY AAA CCC ACA CCA GAM CTG CGC ATC TCC ATC GAG AAC TCC GAA GAG   372
Tyr Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu
    25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 36..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..397
id W31335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..34
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 10..42
id W31335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(151..440)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 64..353
id N30852
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(82..157)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 348..423
id N30852
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 51..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..264
id HSPD03622
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 311..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 262..326
id HSPD03622
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 389..434
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 342..387
id HSPD03622
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 9..323
id AA055130
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 316..375
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 324..383
id AA055130
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 145..436
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 123..414
id H19862
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..110
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 26..86
id H19862
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 107..145
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 84..122
id H19862
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..322
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11.6
seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

AACCCGGTTC AGCTCGCCTT TCTTGGCCAG AGGCGCCGGT TGGACTCACG GCGGGGGC      58
ATG ATG GTG GTG GGT ACG GGC ACC TCG CTG GCG CTC TCC TCC CTC CTG      106
Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu
      -85                      -80                      -75

TCC CTG CTG CTC TTT GCT GGG ATG CAG ATT TAC AGC CGT CAG CTG GCC      154
Ser Leu Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
      -70                      -65                      -60

TCC ACC GAG TGG CTC ACC ATC CAG GGC GGC CTG CTT GGT TCG GGT CTC      202
Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
      -55                      -50                      -45

TTC GTG TTC TCG CTC ACT GCC TTC AAT AAT CTG GAG AAT CTT GTC TTT      250
Phe Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe
      -40                      -35                      -30                      -25

GGC AAA GGA TTC CAA GCA AAG ATC TTC CCT GAG ATT CTC CTG TGC CTC      298
Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
      -20                      -15                      -10

CTG TTG GCT CTC TTT GCA TCT GGC CTC ATC CAC CRA GTC TGT GTC ACC      346
Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
      -5                      1                      5

ACC TGC TTC ATC TTC TCC AGG GTT GGT CTG TAC TAC ATC AAC AAG ATC      394
Thr Cys Phe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile
      10                      15                      20

TCC TCC ACC CTG TAC CAG GCA GCA GCT CCA GTC CTC ACA CCA GCC      439
Ser Ser Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala
      25                      30                      35

```

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..64
id R36288
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 217..251
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 204..238
 id T29670
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 56..112
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 11.6
 seq VFCLLAVAPGAHS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATCCAACAAC CACATCCCTT CTCTACAGAA GCCTCTGAGA AGAAAGTTCT TCACC ATG	58
Met	
GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCT CCA GGT GCT	106
Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly Ala	
-15 -10 -5	
CAC TCC CAG GAA CAA CTG GTG CAG TCT GGG GCT GAG GTG TTG AAG CCT	154
His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys Pro	
1 5 10	
GGG GCC TCA GTG AAC ATT TCC TGC AGG GCA TCT GGG TTC ACC TTC ACC	202
Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe Thr	
15 20 25 30	
AAT TAT TAT GTG CAC TGG GTG CGA CAG GCC CCT GGA CAC GGG CTT GAG	250
Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu	
35 40 45	
TGG ATG GGA GTG ATC AAC CCC GTT AGT GGT TAC ACA AGT TAC GCA CAG	298
Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala Gln	
50 55 60	
AAA CTG CAG GGC AGA CTG ACC ATG ACC ACG GAC ACG GCC GCG AAT ATA	346
Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn Ile	
65 70 75	
GTC TAC ATG GAC CTC AGT AGG CTG AAA TCT GAC GAC ACG GCC GTG TAT	394
Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val Tyr	
80 85 90	
TTC TGT GCG AAA GTG CGG TGT CTT AAG GGG ATA TGC TAT ACA GAG GAT	442
Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu Asp	
95 100 105 110	
GCT CTG GAT CTT TGG	457
Ala Leu Asp Leu Trp	
115	

(2) INFORMATION FOR SEQ ID NO: 118:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 439 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Umbilical cord
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 75..429
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 43..397
 id W31335
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 32..73
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..42
 id W31335
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 33..355
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..323
 id AA055130
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 355..414
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 324..383
 id AA055130
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 56..384
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 28..356
 id AA252648
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 385..428
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 356..399
id AA252648
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 113..439
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 38..364
id AA228934
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..440
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 123..379
id H19862
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 89..149
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 26..86
id H19862
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..184
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 84..122
id H19862
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 23..361
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11.6
seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGTCCGCGG TAAGGCTGAC GC ATG CGC ATA GCT AAC CGC ACC CGG TTC AGC	52
Met Arg Ile Ala Asn Arg Thr Arg Phe Ser	
-110 -105	
TCG CCT TTC TTG GCC AGA GGC GCC GGT TGG ACT CAC GGG CGG GGC ATG	100
Ser Pro Phe Leu Ala Arg Gly Ala Gly Trp Thr His Gly Arg Gly Met	
-100 -95 -90	
ATG GTG GTG GGT ACG GGC ACC TCG CTG GCG CTC TSS TCC CTC CTG TCC	143
Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser	

-85	-80	-75	
CTG CTG CTC TTT GCT GGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC			196
Leu Leu Leu Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser			
-70	-65	-60	
ACC GAG TGG CTC ACC ATC CAG GGC GGC CTG CTT GGT TCG GGT CTC TTC			244
Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe			
-55	-50	-45	-40
GTG TTC TCG CTC ACT GCC TTC AAT AAT CTG GAG AAT CTT GTC TTT GGC			292
Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly			
-35	-30	-25	
AAA GGA TTC CAA GCA AAG ATC TTC CCT GAG ATT CTC CTG TGC CTC CTG			340
Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu			
-20	-15	-10	
TTG GCT CTC TTT GCA TCT GGC CTC ATC CAC CGA GTC TGT GTC ACC ACC			388
Leu Ala Leu Phe Ala Ser Gly Leu Ile His Arg Val Cys Val Thr Thr			
-5	1	5	
TGC TTC ATC TTC TCC ATG GTT GGT CTG TAC TAC ATC AAC AAG ATC TCC			436
Cys Phe Ile Phe Ser Met Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser			
10	15	20	25
TCC			439
Ser			

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..250
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..235
id AA280774
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 246..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 230..266
id AA280774

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..259
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..243
id HUM404F03B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 20..282
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..263
id W05476
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..282
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..262
id R33542
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..282
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 8..278
id T85491
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 151..222
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11.4
seq LMSLLLVLPPVEA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```
ADTCCTGTAA TGGCTGCTTC CTAGAAGGTC GTGTCACGTG GAACCTCTTA ATCTCAGCAT    60
CCGGAGCTCC AGGAAGGGAA AATTTCAAGT CAGATAGAAT TCTATATATA CCATTTCTTT    120
GGAACCTTCA GCCCTCAAGA TTCCAACATC ATG ACC TCA GTT TCA ACA CAG TTG      174
                               Met Thr Ser Val Ser Thr Gln Leu
                               -20
TCC TTA GTC CTC ATG TCA CTG CTT TTG GTG CTG CCT GTT GTG GAA GCA      222
Ser Leu Val Leu Met Ser Leu Leu Leu Val Leu Pro Val Val Glu Ala
-15                               -10                               -5
GTA GAA GCC GGT GAT GCA ATC GCC CTT TTG TTA GGT GTG GTT CTC AGC      270
```

Val Glu Ala Gly Asp Ala Ile Ala Leu Leu Leu Gly Val Val Leu Ser
1 5 10 15
ATT ACA GGC ATT GTG CCT GCT TGG GGG TAT ATG CAY GGG
Ile Thr Gly Ile Val Pro Ala Trp Gly Tyr Met His Gly
20 25

309

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..363
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 60..328
id H19572
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 106..256
id H46195
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 62..115
id H46195
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(207..316)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 183..292
id H46196
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(314..363)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 137..186
id H46196
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(172..212)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 288..328
id H46196
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(237..287)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 239..289
id H19490
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(284..317)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 208..241
id H19490
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(331..363)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 160..192
id H19490
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 263..322
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11.2
seq ILVVLMLPLAQA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

AAGACACGCC TACGATTAGA CTCAGGCAGG CACCTACCGG CGAGCGGCCG CRVGTGACTC 60
CCAGGCGCGG CGGTACCTCA CGGTGGTGAA GGTACAGGG TTGCAGCACT CCCAGTAGAC 120
CAGGAGCTCC GGGAGGCAGG GCCGGCCCCA CGTCCTCTGC GCACCACCCT GAGTTGGATC 180
CTCTGTGCGC CACCCCTGAG TTGGATCCAG GGCTAGCTGC TGTTGACCTC CCCACTCCCA 240

CGCTGCCCTC CTGCCTGCAG CC ATG ACG CCC CTG CTC ACC CTG ATC CTG GTG 292
Met Thr Pro Leu Leu Thr Leu Ile Leu Val
-20 -15

GTC CTC ATG GGC TTA CCT CTG GCC CAG GCC TTG GAC TGC CAC GTG TGT 340
Val Leu Met Gly Leu Pro Leu Ala Gln Ala Leu Asp Cys His Val Cys
-10 -5 1 5

NCC TAC AAC GGA GAC AAC TGC 361
Xaa Tyr Asn Gly Asp Asn Cys
10

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 510 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..372
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..353
id W05519
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 368..423
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 348..403
id W05519
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..260
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 21..264
id T97490
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 231..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 287..347

id T97490
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..315
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..300
id HUML12811
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..275
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..260
id HUML13801
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 139..186
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 11
seq LLALSLLVLWTSP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

AATCCCAGC CTCACATCAC TCACACCTTG CATTTACCCC CTGCATCCCA GTCGCCCTGC	60
AGCCTCACAC AGATCCTGCA CACACCCAGA CAGCTGGCGC TCACACATTC ACCGTTGGCC	120
TGCCTCTGTT CACCTTCC ATG GCC CTG CTA CTG GCC CTC AGC CTG CTA GTT	171
Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val	
-15 -10	
CTC TGG ACT TCC CCA GCC CCA ACT CTG AGT GGC ACC AAT GAT GCT GAA	219
Leu Trp Thr Ser Pro Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu	
-5 1 5 10	
GAC TGC TGC CTG TCT GTG ACC CAG AAA CCC ATC CCT GGG TAC ATC GTG	267
Asp Cys Cys Leu Ser Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val	
15 20 25	
AGG AAC TTC CAC TAC CTT CTC ATC AAG GAT GGC TGC AGG GTG CCT GCT	315
Arg Asn Phe His Tyr Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala	
30 35 40	
GTA GTG TTC ACC ACA CTG AGG GGC CGC CAG CTC TGT GCA CCC CCA GAC	363
Val Val Phe Thr Thr Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp	
45 50 55	
CAG CCC TGG GTA GAA CGC ATC ATC CAG AGA CTG CAG AGG ACC TCA GCC	411
Gln Pro Trp Val Glu Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala	
60 65 70 75	
AAG ATG AAR MGC CGM AGC AGT KAA CCT ATG AMC GTG MAG AGG GAR CCG	459
Lys Met Lys Xaa Arg Ser Ser Xaa Pro Met Xaa Val Xaa Arg Glu Pro	

80

85

90

GAG TCC GAG TCA AGC ATT GTG AAT KAT TAC CTA MCT GGG GAA CGA RGA 507
Glu Ser Glu Ser Ser Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa
95 * 100 105

AGG 510
Arg

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 91..226
id W60940
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 48..100
id W60940
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..106
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..47
id W60940
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 90..254
id H39980
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..99
id H39980
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 308..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 247..323
id H39980
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(148..292)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 282..426
id N41026
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(283..384)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 191..292
id N41026
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..160
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 8..102
id R49793
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 199..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 141..213
id R49793
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 152..199
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 93..140
id R49793

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..160
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..143
id W74783
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 190..253
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 173..236
id W74783
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 74..136
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10.5
seq RLLLLPLLLAVSG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```
AATTTCACTT GCCTGGACGC TGCGCCACAT CCCACCGGCC CTTACACTGT GGTGTCCAGC      60
AGCATCCGGC TTC ATG GGG GGA CTT GAA CCC TGC AGC AGG CTC CTG CTC      109
      Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu
      -20                      -15                      -10

CTG CCT CTC CTG CTG GCT GTA AGT GGT CTC CGT CCT GTC CAG GCC CAG      157
Leu Pro Leu Leu Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln
      -5                      1                      5

GCC CAG AGC GAT TGC AGT TGC TCT ACG GTG AGC CCG GGC GTG CTG GCA      205
Ala Gln Ser Asp Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala
      10                      15                      20

GGG ATC GTG ATG GGA GAC CTG GTG CTG ACA GTG CTC ATT GCC CTG GCC      253
Gly Ile Val Met Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala
      25                      30                      35

GTG TAC TTC CTG GGC CGG CTG GTC CCT CGG GGG CGA GGG GCT GCG GAG      301
Val Tyr Phe Leu Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu
      40                      45                      50                      55

GCA SNG ACC CGG AAA CAG CGT ATC ACT GAG ACC GGG TCG CCT TAT CAG      349
Ala Xaa Thr Arg Lys Gln Arg Ile Thr Glu Thr Gly Ser Pro Tyr Gln
      60                      65                      70

GAG CTC CAG GGT CAG AGG TCG GAT GTC TAC AGC      382
Glu Leu Gln Gly Gln Arg Ser Asp Val Tyr Ser
      75                      80
```

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..196
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 13..155
id N41450
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 153..292
id N41450
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 327..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 288..386
id N41450
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..332
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 202..330
id W76359
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 54..124
id W76359
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..54
id W76359
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 327..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 326..369
id W76359
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..196
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 162..194
id W76359
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 132..162
id W76359
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 46..120
id W04321
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..47
id W04321
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 153..190
id W04321

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..163
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 115..153
id W04321
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..124
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 12..134
id AA025985
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 200..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 208..294
id AA025985
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 366..425
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 381..440
id AA025985
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..166
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 145..176
id AA025985
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 208..306
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 146..244
id H09017
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..126
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..65
id H09017
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 327..368
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 267..308
id H09017
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 178..249
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10
seq LCRALCLFPRVFA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

AAAGGACTCC AAAGCGAGGC CGGGGACTGA AGGTGTGGGT GTCGAGCCCT CTGGCAGAGG      60
GTTAACCTGG GTCAAATGCA CGGATTCTCA CCTCGTACAG TTACGCTCTC CCGCGGCACG      120
TCCGCGAGGA CTTGAAGTCC TGAGCGCTCA AGTTTGTCCG TAGGTCGAGA GAAGGCC          177
ATG GAG GTG CCG CCA CCG GCA CCG CGG AGC TTT CTC TGT AGA GCA TTG          225
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
      -20                      -15                      -10
TGC CTA TTT CCC CGA GTC TTT GCT GCC GAA GCT GTG ACT GCC GAT TCG          273
Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
      -5                      1                      5
GPA GTC CTT GAG GAG CGT CAG AAG CGG CTT CCC TAC STC CCA GAG CCC          321
Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Xaa Pro Glu Pro
      10                      15                      20
TAT TAC CGG AAT CTG GAT GGG ACC GCC TCC GGG AGC TGT TTK GCA AAG          369
Tyr Tyr Arg Asn Leu Asp Gly Thr Ala Ser Gly Ser Cys Xaa Ala Lys
      25                      30                      35
ATG AAC AGC AGA GAA TTT CAA AGG ACC TTG CTA ATA TCT GTA AGA CGG          417
Met Asn Ser Arg Glu Phe Gln Arg Thr Leu Leu Ile Ser Val Arg Arg
      45                      50                      55
CAG CTA
Gln Leu
      423

```

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 8..208

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..201
id N56128
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 242..311

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 233..302
id N56128
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 207..244

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 199..236
id N56128
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 19..113

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..95
id N87312
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 223..286

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 208..271
id N87312
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 181..222

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92
region 165..206
id N87312
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 46..270
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..225
 id R57616
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 51..241
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..191
 id AA093451
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 75..131
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.5
 seq LMCLSLCTAFALS/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

AGAGCTGAGC CGGTGGGTGA GCGGCGGCCA CGGCATCCTG TGCTGTGGGG GCTACGAGGA      60
AAGATCTAAT TATC  ATG  GAC  CTG  CGA  CAG  TTT  CTT  ATG  TGC  CTG  TCC  CTG      110
          Met Asp Leu Arg  Gln Phe Leu Met Cys Leu Ser Leu
                               -15                               -10

TGC  ACA  GCC  TTT  GCC  TTG  AGC  AAA  CCC  ACA  GAA  AAG  AAG  GAC  CGT  GTA      158
Cys Thr Ala Phe Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val
          -5                               1                               5

CAT  CAT  GAG  CCT  CAG  CTC  AGT  GAC  AAG  GTT  CAC  AAT  GAT  GCT  CAG  AGT      206
His His Glu Pro Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser
          10                               15                               20                               25

TTT  GWT  TAT  GAC  CAT  GAT  GCC  TTC  TTG  GGT  GCT  GAA  GAA  GCA  AAG  ASM      254
Phe Xaa Tyr Asp His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa
                               30                               35                               40

TTT  GAT  CAG  CTG  ACA  CCA  GAA  GAG  AGC  AAG  GAA  AGG  CTT  GGA  AAG  ATT      302
Phe Asp Gln Leu Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile
                               45                               50                               55

GTA  AGT  AAR  ATM  GAT  GGC  GAC  AAG  GAC  GGG  TTT  GTC  ACT  GTG  GAT  GAG      350
Val Ser Lys Ile Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu
          60                               65                               70

CTC  AAA
Leu Lys
          75

```

.2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..320
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 17..287
id R35366
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..320
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..288
id R35909
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..286
id R20566
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..320
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 10..288
id H09254
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..320
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 10..288
id R25274
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 24..113

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.5
seq LLFLSQFCILSGG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

AAAAGTGC GC AGGCGCTGGC AAG ATG GCG GGA GGG GTG CGC CCG CTG CGG GGC      53
      Met Ala Gly Gly Val Arg Pro Leu Arg Gly
      -30                               -25

CTC CGC GCC TTG TGT CGC GTG CTG CTC TTC CTC TCG CAG TTC TGC ATT      101
Leu Arg Ala Leu Cys Arg Val Leu Leu Phe Leu Ser Gln Phe Cys Ile
-20                               -15                               -10                               -5

CTG TCG GGC GGT GAA AGT ACT GAA ATC CCA CCT TAT GTG ATG AAG TGT      149
Leu Ser Gly Gly Glu Ser Thr Glu Ile Pro Pro Tyr Val Met Lys Cys
      1                               5                               10

CCG AGC AAT GGT TTG TGT AGC AGG CTT CCT GCA GAC TGT ATA GAC AGC      197
Pro Ser Asn Gly Leu Cys Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser
      15                               20                               25

ACA ACA AAT TTC TCC TGT ACC TAT GGG AAG CCT GTM ACT TTT GAC TGT      245
Thr Thr Asn Phe Ser Cys Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys
      30                               35                               40

RCA GTG AAA CCA TCT GTT ACC TGT GTT GAT CAA GAC TTC AAA TCC CAA      293
Xaa Val Lys Pro Ser Val Thr Cys Val Asp Gln Asp Phe Lys Ser Gln
      45                               50                               55                               60

AAG RAC TTC ATC ATT AAC ATG ACT TGC      320
Lys Xaa Phe Ile Ile Asn Met Thr Cys
      65

```

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..198)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 2..198
id N27605
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: complement(2..69)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..68
 id N78549
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 36..98
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.3
 seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

AAAATGCTTT CGGTAGGCAC TCCAMGGCTG TRAAG ATG GCG GCG GCT GCG TGG	53
Met Ala Ala Ala Ala Trp	
-20	
CTT CAG GTG TTG CCT GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA	101
Leu Gln Val Leu Pro Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser	
-15 -10 -5 1	
CCA CTG TCG TTT TTC AGT GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC	149
Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala Thr Val Ala Ala Ala Asp	
5 10 15	
CGG TCC AAA TGG CAC ATT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT	197
Arg Ser Lys Trp His Ile Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser	
20 25 30	
TTT GGA AHK ATC CTC TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT	245
Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp	
35 40 45	
GGA GAA CCT TGT GAC CTG TCT TTG AAT ATA AYM TGG TAT CTG AAA AGC	293
Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile Xaa Trp Tyr Leu Lys Ser	
50 55 60 65	
GCT GAT TGT TAC AAT GAA ATC TAT AAC TTC AAG GCA GAA GAA GTA GAG	341
Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu	
70 75 80	
TTG TAT TTG GAA AAA CTT AAG GAA AAA AGA GGC TTG TCT GGG AAA TGG	389
Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg Gly Leu Ser Gly Lys Trp	
85 90 95	

(x) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..267
id HSC1WH101
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 134..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 41..204
id R12437
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..136
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..42
id R12437
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..203
id R13448
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 244..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 82..135
id T69236
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 197..244
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 36..83
id T69236
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 212..268
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 9.3
 seq LLWLALACSPVHT/XL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

ATCCGGCGCG CTGGAGCGTT TTCCGGCCGT GCGTTTGTGG CCGTCCGGCC TCCCTGACAT   60
GCAGATTTCC ANSSAGAAGA CAGAGAAGGA GCNAGTGGTC ATGGAATGGG CTGGGGTCAA   120
AGACTGGGTG CCTGGGAGCT GAGGCAGCCA CCGTTTCAGC CTGGCCAGCC CTCTGGACCC   180
CGAGGTTGGA CCCTACTGTG ACACACCTAC C ATG CGG ACA CTC TTC AAC CTC       232
                                   Met Arg Thr Leu Phe Asn Leu
                                   -15
CTC TGG CTT GCC CTG GCC TGC AGC CCT GTT CAC ACT ASC CTG TCA AAG       280
Leu Trp Leu Ala Leu Ala Cys Ser Pro Val His Thr Xaa Leu Ser Lys
   -10                               -5                               1
TCA GAT GCC VSA AAA CCG CCT AGG                                     304
Ser Asp Ala Xaa Lys Pro Pro Arg
   5                               10

```

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Muscle

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 43..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 29..148
 id T98462
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 179..216
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 165..202
 id T98462
 est

(ix) FEATURE:

- (A) NAME/KEY: other
 - (B) LOCATION: 17..162
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 98
region 110..255
id T82829
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 16..162
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 1..147
id AA027213
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 32..162
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 99
region 2..132
id AA095731
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: 179..216
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 92
region 149..186
id AA095731
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: complement(85..162)
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 97
region 358..435
id AA027214
est
- (ix) FEATURE:
- (A) NAME/KEY: other
 - (B) LOCATION: complement(16..87)
 - (C) IDENTIFICATION METHOD: blastn
 - (D) OTHER INFORMATION: identity 91
region 434..505
id AA027214
est
- (ix) FEATURE:
- (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 37..84
 - (C) IDENTIFICATION METHOD: Von Heijne matrix
 - (D) OTHER INFORMATION: score 9.3
seq LFVAIFAVPLILG/QE
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

CTTTTTTACT TTCACAGCAA TAGTGCAGAA TCCAGA ATG GAT GTC CTC TTT GTA      54
                               Met Asp Val Leu Phe Val
                               -15

GCC ATC TTT GCT GTG CCA CTT ATC CTG GGA CAA GAA TAT GAG GAT GAA      102
Ala Ile Phe Ala Val Pro Leu Ile Leu Gly Gln Glu Tyr Glu Asp Glu
-10                -5                1                5

GAA AGA CTG GGA GAG GAT GAA TAT TAT CAG GTG GTC TAT TAT TAT ACA      150
Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln Val Val Tyr Tyr Tyr Thr
                10                15                20

GTC ACC CCC ATT ATG ATG RCY TTA GGG MCR RAT TTC ACC ATT GAT TAC      198
Val Thr Pro Ile Met Met Xaa Leu Gly Xaa Xaa Phe Thr Ile Asp Tyr
                25                30                35

KCC ATA TTT GAG TCA GAG                                          216
Xaa Ile Phe Glu Ser Glu
                40

```

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..181)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 3..181
id N27605
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(3..53)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..51
id N78549
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 20..82
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3

seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

AAACTCCACG GCTGTGAAG ATG GCG GCT GCT GCG TGG CTT CAG GTG TTG CCT	52
Met Ala Ala Ala Trp Leu Gln Val Leu Pro	
-20 -15	
GTC ATT CTT CTG CTT CTG GGA GCT CAC CCG TCA CCA CTG TCG TTT TTC	100
Val Ile Leu Leu Leu Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe	
-10 -5 1 5	
AGT GCG GGA CCG GCA ACC GTA GCT GCT GCC GAC CGG TCC AAA TGG CAC	148
Ser Ala Gly Pro Ala Thr Val Ala Ala Asp Arg Ser Lys Trp His	
10 15 20	
ATT CCG ATA CCG TCG GGG AAA AAT TAT TTT AGT TTT GGA AAG ATC CTC	196
Ile Pro Ile Pro Ser Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu	
25 30 35	
TTC AGA AAT ACC ACT ATC TTC CTG AAG TTT GAT GGA GAA CCT TGT GAC	244
Phe Arg Asn Thr Thr Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp	
40 45 50	
CTG TCT TTG AAT ATA ACC TGG TAT CTG AAA AGC GCT GAT TGT TAC AAT	292
Leu Ser Leu Asn Ile Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn	
55 60 65 70	
GAA ATC TAT AAC TTC AAG GCA GAA GAA GTA GAG TTG TAT TTG GAA AAA	340
Glu Ile Tyr Asn Phe Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys	
75 80 85	
CTT	343
Leu	

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 48..243
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 72..267
id R13448
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 126..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 82..211
id T69236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 79..126
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 36..83
id T69236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..244
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 73..269
id R12437
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..211
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 136..299
id HSC1WH101
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..50
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..34
id HSC1WH101
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..150
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9.2
seq LLXLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

AGCGTTTTCG GGCCTGCGT TTGTGGCCGT CCGGCCTCCC TGACATGCAG CCCTCTGGAC 60

CCCGAGGTTG GACCCTACTG TGACACACCT ACC ATG CGG ACA CTC TTC AAC CTC 114
Met Arg Thr Leu Phe Asn Leu

-15

CTC	TKG	CTT	GCC	CTG	GCC	TGC	AGC	CCT	GTT	CAC	ACT	ACC	CTG	TCA	AAG	162
Leu	Xaa	Leu	Ala	Leu	Ala	Cys	Ser	Pro	Val	His	Thr	Thr	Leu	Ser	Lys	
		-10					-5						1			
TCA	GAT	GCC	AAA	AAA	GCC	GCC	TCA	AAG	ACG	CTG	CTG	GAG	AAG	AGT	CAG	210
Ser	Asp	Ala	Lys	Lys	Ala	Ala	Ser	Lys	Thr	Leu	Leu	Glu	Lys	Ser	Gln	
5					10					15					20	
TTT	TCA	GAT	AAG	CCG	GTG	CAA	GAC	CGG	GGT	TTG	GTG	GTG	ACG	GAC	GGG	258
Phe	Ser	Asp	Lys	Pro	Val	Gln	Asp	Arg	Gly	Leu	Val	Val	Thr	Asp	Gly	
				25					30					35		

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 8..198
id R72126
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 8..175
id W60037
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..174
id W24729
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 228..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 209..252
id W24729
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..174
id R74426
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 228..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 209..252
id R74426
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..174
id H42031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 228..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 209..252
id H42031
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..181
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 9
seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```
ACTGAAGTGG GCAAAATCCC CGAGAAGCAG CGGTGTCCCC AGCCTCTCAC TCGGAGCCGA      60
T ATG GGG AGT AAA GTG GCG GAC CTG CTG TAC TGG AAG GAC ACG AGG ACG      109
Met Gly Ser Lys Val Ala Asp Leu Leu Tyr Trp Lys Asp Thr Arg Thr
-40              -35              -30              -25

TCA GGA GTG GTC TTC ACA GGC CTG ATG GTC TCC CTC CTC TGC CTC CTG      157
Ser Gly Val Val Phe Thr Gly Leu Met Val Ser Leu Leu Cys Leu Leu
-20              -15              -10

CAC TTT AGC ATC GTG TCC GTG GCC GCG SAC TTT GGS YCK KKT DSY WGM      205
```

His Phe Ser Ile Val Ser Val Ala Ala Xaa Phe Gly Xaa Xaa Xaa Xaa
-5 1 5

YTK GGG GMA CAA TCC TCT YTC AGG GTT TAC GCA AAG TGC TGC AGG CCG 253
Xaa Gly Xaa Gln Ser Ser Xaa Arg Val Tyr Ala Lys Cys Cys Arg Pro
10 15 20

TGC ACC GGG GGG ATG GAG 271
Cys Thr Gly Gly Met Glu
25 30

(2) INFORMATION FOR SEQ ID NO: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..101
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 14..114
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..164
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 111..176
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 163..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 174..240
id N87112
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..229
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..195
id AA206940

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 35..229
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..195
id AA186993
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..229
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..193
id T68050
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..178
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..147
id AA157180
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 175..231
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 146..202
id AA157180
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 28..114
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
seq ALLIVCDVPSASA/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```
TCACCTTATAG AAGGGAGAGG AGCGAAC ATG GCA GCG CGT TGG CGG TTT TGG TGT    54
                               Met Ala Ala Arg Trp Arg Phe Trp Cys
                               -25

GTC TCT GTG ACC ATG GTG GTG GCG CTG CTC ATC GTT TGC GAC GTT CCC    102
Val Ser Val Thr Met Val Val Ala Leu Leu Ile Val Cys Asp Val Pro
-20          -15          -10          -5

TCA GCC TCT GCC CAA AGA AAG AAG GAG ATG GTG TTA TCT GAA AAG GTT    150
Ser Ala Ser Ala Gln Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val
          1          5          10

AGT CAG CTG ATG GAA TGG ACT AAC AAA AGA CCT GTA ATA AGA ATG AAT    198
```

Ser Gln Leu Met Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn
15 20 25
GGA GAC AAG TTC CGT CGC CTT GTG AAG CCC CAC ATG
Gly Asp Lys Phe Arg Arg Leu Val Lys Pro His Met
30 35 40

234

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 186..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..81
id AA089592
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 266..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 81..127
id AA089592
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 385..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..224
id AA089592
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(305..440)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 211..346
id R83736
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: complement(294..439)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 202..347
 id R83667
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 30..86
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.8
 seq SAVLSGFVLGALA/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

AACTCTTG	GTG	TAGCCTG	GAGG	CGGCGGT	AS	ATG	GAG	GGG	GAG	AGT	ACG	TCG	GCG	53		
						Met	Glu	Gly	Glu	Ser	Thr	Ser	Ala			
														-15		
GTG	CTC	TCG	GGC	TTT	GTG	CTC	GGC	GCA	CTC	GCT	TTC	CAG	CAC	CTC	AAC	101
Val	Leu	Ser	Gly	Phe	Val	Leu	Gly	Ala	Leu	Ala	Phe	Gln	His	Leu	Asn	
	-10					-5					1				5	
ACG	GAC	TCG	GAC	ACG	GAA	GGT	TTT	CTT	CTT	GGG	GAA	GTA	AAA	GGT	GAA	149
Thr	Asp	Ser	Asp	Thr	Glu	Gly	Phe	Leu	Leu	Gly	Glu	Val	Lys	Gly	Glu	
				10					15					20		
GCC	AAG	AAC	AGC	ATT	ACT	GAT	TCC	CAA	ATG	GAT	GAT	GTT	GAA	GTT	GTT	197
Ala	Lys	Asn	Ser	Ile	Thr	Asp	Ser	Gln	Met	Asp	Asp	Val	Glu	Val	Val	
			25					30					35			
TAT	ACA	ATT	GAC	ATT	CAG	AAA	TAT	ATT	CCA	TGC	TAT	CAG	CTT	TTT	AGC	245
Tyr	Thr	Ile	Asp	Ile	Gln	Lys	Tyr	Ile	Pro	Cys	Tyr	Gln	Leu	Phe	Ser	
		40					45					50				
TTT	TAT	AAT	TCT	TCA	GGC	GAA	GTA	AAT	GAG	CAA	GCA	CTG	AAG	AAA	ATA	293
Phe	Tyr	Asn	Ser	Ser	Gly	Glu	Val	Asn	Glu	Gln	Ala	Leu	Lys	Lys	Ile	
	55					60					65					
TTA	TCA	AAT	GTC	AAA	AAG	AAT	GTG	GTA	GGT	TGG	TAC	AAA	TTC	CGT	CGT	341
Leu	Ser	Asn	Val	Lys	Lys	Asn	Val	Val	Gly	Trp	Tyr	Lys	Phe	Arg	Arg	
	70				75				80					85		
CAT	TCA	GAT	CAG	ATC	ATG	ACG	TTT	AGA	GAG	AGG	YTG	CTT	CAC	AAA	AAC	389
His	Ser	Asp	Gln	Ile	Met	Thr	Phe	Arg	Glu	Arg	Leu	Leu	His	Lys	Asn	
				90					95					100		
TTG	CAG	GAG	CAT	TTT	TCA	AAC	CAA	GAC	CTT	GTT	TTT	CTG	CTA	TTA	ACA	437
Leu	Gln	Glu	His	Phe	Ser	Asn	Gln	Asp	Leu	Val	Phe	Leu	Leu	Leu	Thr	
			105					110					115			
CCA																440
Pro																

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 45..258
id H81225
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..39
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..38
id H81225
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..216
id AA044118
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..225
id W01412
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 13..226
id W42797
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 95..230
id R39635
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..124
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 15..94
id R39635
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..201
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.8
seq VPMLLLIVGGSFG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```
AAAGTGAGTT AAGGACGTAC TCGTCTTGGT GAGAGCGTGA STGCTGAGAT TTGGGAGTCT    60
GCGCTAGGCC CGCTTGGAGT TCTGAGCCGA TGGAAGAGTT CACTC ATG TTT GCA CCC    117
                               Met Phe Ala Pro
                               -30

GCG GTG ATG CGT GCT TTT CGC AAG AAC AAG ACT CTC GGC TAT GGA GTC    165
Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu Gly Tyr Gly Val
-25                               -20                               -15

CCC ATG TTG TTG CTG ATT GTT GGA GGT TCT TTT GGT CTT CGT GAG TTT    213
Pro Met Leu Leu Leu Ile Val Gly Ser Phe Gly Leu Arg Glu Phe
-10                               -5                               1

TCT CAA ATC CGA TAT GAT GCT GTG AAG AGT AAA ATG GAT CCT GAG CGG    261
Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met Asp Pro Glu Arg
5                               10                               15                               20
```

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 440 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 143..345
(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 113..315
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 335..442
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 304..411
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..149
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 43..120
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 44..317
id HUM172D06B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 372..442
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 340..410
id HUM172D06B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 35..73
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 8..46
id HUM172D06B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 153..442
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 125..414
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 77..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..119
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..412
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 45..385
id HUM159G08B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..73
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..47
id HUM159G08B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 143..367
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 92..316
id N34957
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 80..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 30..97
id N34957
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 362..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 312..379
id N34957
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..431
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.7
seq AVALSFLGLWGA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

AAGAGAAAGT GTCGGTCTCC AAG ATG GCG GCC GCC TGG CSD TCT GGT CCG TCT   53
              Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser
              -135                      -130

GCT CCG GAG GCC GTG ACG GCC AGA CTC GTT GGT GTC CTG TGG TTC GTC   101
Ala Pro Glu Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val
-125                      -120                      -115

TCA GTC ACT ACA GGA CCC TGG GGG GCT GTT GCC ACC TCC GCC GGG GGC   149
Ser Val Thr Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly
-110                      -105                      -100                      -95

GAG GAG TCG CTT AAG TGC GAG GAC CTC AAA GTG GGA CAA TAT ATT TGT   197
Glu Glu Ser Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys
              -90                      -85                      -80

AAA GAT CCA AAA ATA AAT GAC GCT ACG CAA GAA CCA GTT AAC TGT ACA   245
Lys Asp Pro Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr
              -75                      -70                      -65

AAC TAC ACA GCT CAT GTT TCC TGT TTT CCA GCA CCC AAC ATA ACT TGT   293
Asn Tyr Thr Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys
              -60                      -55                      -50

AAG GAT TCC AGT GGC AAT GAA ACA CAT TTT ACT GGG AAC GAA GTT GGT   341
Lys Asp Ser Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly
-45                      -40                      -35

TTT TTC AAG CCC ATA TCT TGC CGA AAT GTA AAT GGC TAT TCC TAC AAA   389
Phe Phe Lys Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys
-30                      -25                      -20                      -15

GTG GCA GTC GCA TTG TCT CTT TTT CTT GGA TGG TTG GGA GCA GAT CGA   437
Val Ala Val Ala Leu Ser Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg
              -10                      -5                      1

TTT
Phe
440

```

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..165
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 136..274
id HSC1WH101
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 73..211
id R12437
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 72..210
id R13448
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 105..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 82..142
id T69236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 58..105
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 36..83
id T69236
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 73..129
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.6
seq LLWLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
AGTGGCCGTC CGGCCTCNCT GACATGCAGC CCTCTGGACC CCGAGGTTGG ACCCTACTGT    60
GACACACCTA CC ATG CGG ACA CTC TTC AAC CTC CTC TGG CTT GCC CTG GCC    111
      Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala
                        -15                                -10

TGC AGC CCT GTT CAC ACT ACC CTG TCA AAG TCA GAT GCC AAA AAA GCC    159
Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala
      -5                      1                      5                      10

ACC TCA GGG                                                    168
```

Thr Ser Gly

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..381
id C15922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 224..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 200..328
id AA100508
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..225
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 96..200
id AA100508
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..90
id AA100508
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..353
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 89..421
id W27023

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 353..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 422..463
id W27023
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 76..245
id W68781
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 267..361
id W68781
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..69
id W68781
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 176..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 101..331
id T80234
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 62..102
id T80234
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..37
id T80234
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 132..257
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6
seq ASLFLLLSLTVFS/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

AAGAGGAGAC TGCAGACTTC GGTGAGGAA ACGGGTATTT CATGTCTCAG GGAGTAGGTT      60
TGTGCAGTTA CAGCTTTTCT GTTGGTATGC ATAATTAATA ATTGGAGCTG CAAAGCAGAT    120
CGTGACAAGA G ATG GAC GGT CAG AAG AAA AAT TGG AAG GAC AAG GTT GTT      170
           Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val
                   -40                               -35                   -30

GAC CTC CTG TAC TGG AGA GAC ATT AAG AAG ACT GGA GTG GTG TTT GGT      218
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
           -25                               -20                   -15

GCC AGC CTA TTC CTG CTG CTT TCA TTG ACA GTA TTC AGC ATT GTG AGC      266
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
           -10                               -5                               1

GTA ACA GCC TAC ATT GCC TTG GCC CTG CTC TCT GTG ACC ATC AGC TTT      314
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
           5                               10                               15

AGG ATA TAC AAG GGT GTG ATC CAA GCT ATC CAG AAA TCA GAT GAA GGC      362
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
           20                               25                               30                               35

CAC CCA TTC AGG GCA TAT CTG GAA TCT GAA GTT GCT ATA TCT      404
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser
           40                               45

```

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 439..475

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 24..60
 id AA013254
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 41..94
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.5
 seq LVLGLVPLILWA/DR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

AACTTTCCCA GTCCTAGGCG GCGGTCAGAT CCTTGCAAGC ATG GTC GCG CCG GGG      55
                                   Met Val Ala Pro Gly
                                   -15

CTT GTA CTC GGG CTG GTG CTG CCA TTA ATC CTG TGG GCC GAC AGA AGT      103
Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu Trp Ala Asp Arg Ser
-10                               -5                               1

GCA GGT ATT GGT TTT CGC TTT GCT TCA TAC ATC AAT AAT GAT ATG GTG      151
Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile Asn Asn Asp Met Val
5                               10                               15

CTG CAG AAG GAG CCT GCT GGG GCA GTG ATA TGG GGC TTC GGT ACA CCT      199
Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp Gly Phe Gly Thr Pro
20                               25                               30                               35

GGA GCC ACA GTG ACC GTG ACC CTG CGC CAA GGT CAG GAA ACC ATC ATG      247
Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly Gln Glu Thr Ile Met
40                               45                               50

AAG AAA GTG ACC AGT GTG AAA GCT CAC TCT GAT ACG TGG ATG GTG GTA      295
Lys Lys Val Thr Ser Val Lys Ala His Ser Asp Thr Trp Met Val Val
55                               60                               65

CTG GAT CCT ATG AAG CCT GGA GGR SCT TTC GAA GTG ATG GCA CAA CAG      343
Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu Val Met Ala Gln Gln
70                               75                               80

ACT TTG GAG AAA ATA AAC TTC ACC CTG AGA GTT CAT GAC GTC CTG TTT      391
Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val His Asp Val Leu Phe
85                               90                               95

GGA GAT GTC TGG CTC TGT AGT GGG CAG AGT AAC ATG CAG ATG ACC GCG      439
Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn Met Gln Met Thr Ala
100                               105                               110                               115

CGG GTC TTC AGA TGG CGT CAT GTG KTG GGG CTT TTA                      475
Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu Leu
120                               125

```

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 82..357
id AA075901
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..298
id H25630
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 3..298
id H43485
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..285
id H80718
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..318
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 28..303
id AA044211
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..107
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5

seq LLTIVGLILPTRG/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

ACCTCTCTCC ACGAGGCTGC CGGCTTAGGA CCCCCAGCTC CGAC ATG TCG CCC TCT      56
                               Met Ser Pro Ser
                               -20

GGT CGC CTG TGT CTT CTC ACC ATC GTT GGC CTG ATT CTC CCC ACC AGA      104
Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg
-15                               -10                               -5

GGA CAG ACG TTG AAA GAT ACC ACG TCC AGT TCT TCA GCA GAC TCA ACT      152
Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr
  1                               5                               10                               15

ATC ATG GAC ATT CAG GTC CCG ACA CGA GCC CCA GAT GCA GTC TAC ACA      200
Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr
                20                               25                               30

GAA CTC CAG CCC ACC TCT CCA ACC CCA ACC TGG CCT GCT GAT GAA ACA      248
Glu Leu Gln Pro Thr Ser Pro Thr Pro Thr Trp Pro Ala Asp Glu Thr
                35                               40                               45

CCA CAA CCC CAG ACC CAG ACC CAG CAA CTG GAA GGA ACG GAT GGG CCT      296
Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro
                50                               55                               60

CTA GTG ACA GAT CCA GAG ACA CCA CGG                                323
Leu Val Thr Asp Pro Glu Thr Pro Arg
  65                               70

```

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 43..330
id W31335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..63

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..42
id W31335
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..352
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 2..326
id AA094921
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 23..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..323
id AA055130
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..183
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 60..181
id R16450
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 180..245
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 179..244
id R16450
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 18..61
id R16450
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..183
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 75..192
id H94808
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 197..254
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 208..265
 id H94808
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 13..153
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.3
 seq LALSSLLSLLLFA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

AAGCGCTGAC GC ATG CGC ATA GCT AAC CGC ACC CGG TTC AGC TTG CCT TTC      51
      Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe
            -45                      -40                      -35

TTG GCC AGA GGC GCC GGT TGG ACT CAC GGG CGG GGC ATG ATG GTG GTG      99
Leu Ala Arg Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val
            -30                      -25                      -20

GGT ACG GGC ACC TCG CTG GCG CTC TCC TCC CTC CTG TCC CTG CTG CTC     147
Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu
            -15                      -10                      -5

TTT GCT GGG ATG CAG ATG TAC AGC CGT CAG CTG GCC TCC ACC GAG TGG     195
Phe Ala Gly Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp
            1                      5                      10

CTC ACC ATC CAG GGC GGC CTG CTT GGT TCG GGT CTC TTC GTG TTC TCG     243
Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser
            15                      20                      25                      30

CTC ACT GCC TTC AAT AAT CTG GAG AAT CTT GTC TTT GGC AAA GGA TTC     291
Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe
            35                      40                      45

CAA GCA AAG ATC TTC CCT GAG ATT CTC CTG TGC CTC CTG TTG GCT CTC     339
Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Ala Leu
            50                      55                      60

TTT GCA TCT GGC CCG                                             354
Phe Ala Ser Gly Pro
            65
  
```

(2) INFORMATION FOR SEQ ID NO: 141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..209
id R54127
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 221..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 199..295
id R54127
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 10..303
id R60167
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..230
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..205
id H29628
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 211..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 185..291
id H29628
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 85..289
id N40052
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 28..116
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..89
 id N40052
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 24..230
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 10..216
 id R34889
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 221..279
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 206..264
 id R34889
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 62..166
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.3
 seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```

ATCTGTGCTG CTGGCCTGGG GTTGTGGTTG AGGCCGTGTC TCCGCTCCTG TGCCCGGGAA      60
G  ATG  GTG  CTA  GGT  GGT  TGC  CCG  GTT  AGT  TAC  TTA  CTT  CTG  TGC  GGC  CAG      109
  Met  Val  Leu  Gly  Gly  Cys  Pro  Val  Ser  Tyr  Leu  Leu  Leu  Cys  Gly  Gln
  -35                -30                -25                -20

GCG  GCT  TTG  CTG  CTG  GGG  AAT  TTA  CTT  CTG  CTG  CAT  TGT  GTG  TCT  CGG      157
Ala  Ala  Leu  Leu  Leu  Gly  Asn  Leu  Leu  Leu  Leu  His  Cys  Val  Ser  Arg
          -15                -10                -5

AGC  CAC  TCG  CAA  AAT  GCG  ACC  GCT  GAG  CCT  GAG  CTC  ACA  TCC  GCT  GGC      205
Ser  His  Ser  Gln  Asn  Ala  Thr  Ala  Glu  Pro  Glu  Leu  Thr  Ser  Ala  Gly
          1                5                10

GCC  GCC  CAG  CCG  GAG  GGC  CCC  GGG  GGT  GCT  GCG  AGC  TGG  GAA  TAT  GGC      253
Ala  Ala  Gln  Pro  Glu  Gly  Pro  Gly  Gly  Ala  Ala  Ser  Trp  Glu  Tyr  Gly
          15                20                25

GAC  CCC  CAC  TCT  CCG  GTC  ATC  CTC  TGM  TCT  TAC  CTA  CCT  GAT  GAA  TTT      301
Asp  Pro  His  Ser  Pro  Val  Ile  Leu  Xaa  Ser  Tyr  Leu  Pro  Asp  Glu  Phe
          30                35                40                45

ATA  GAA  TGT  GAA  GAC  CGG
Ile  Glu  Cys  Glu  Asp  Arg
          50
  
```

(2) INFORMATION FOR SEQ ID NO: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..234
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 263..319
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 340..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 318..365
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 232..268
id T59284
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..291
id W52428
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 361..453
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 298..390
 id W52428
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 79..237
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 8.1
 seq IYALFLLVGVCVA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

AAGTAAATAA TCTCGGAAAG GCGAGAAAGA AGCTGTCTCC ATCTTGTCTG TATCCGCTGC      60
TCTTGTGACG TTGTGGAG ATG GGG AGC GTC CTG GGG CTG TGC TCC ATG GCG      111
                Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala
                -50                                -45
AGC TGG ATA CCA TGT TTG TGT GGA AGT GCC CCG TGT TTG CTA TGC CGA      159
Ser Trp Ile Pro Cys Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg
        -40                                -35                                -30
TGC TGT CCT AGT GGA AAC AAC TCC ACT GTA ACT AGA TTG ATC TAT GCA      207
Cys Cys Pro Ser Gly Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala
        -25                                -20                                -15
CTT TTC TTG CTT GTT GGA GTA TGT GTA GCN TGT GTA ATG TTG ATA CCA      255
Leu Phe Leu Leu Val Gly Val Cys Val Ala Cys Val Met Leu Ile Pro
        -10                                -5                                1                                5
GGA ATG GAA GAA CAA CTG AAT AAG ATT CCT GGA TTT TGT GAG AAT GAG      303
Gly Met Glu Glu Gln Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu
                10                                15                                20
AAA GGT GTT GTC CCT TGT AAC ATT TTG GTT GGC TAT AAA GCT GTA TAT      351
Lys Gly Val Val Pro Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr
                25                                30                                35
CGT TTG TGC TTT GGT TTG GCT ATG HTC TAT CTT CTT CTC TCT TTA CTA      399
Arg Leu Cys Phe Gly Leu Ala Met Xaa Tyr Leu Leu Leu Ser Leu Leu
        40                                45                                50
ATG ATC AAA GTG AAG AGT AGC AGT GAT CCT AGA GCT GCA GTG CAC AAT      447
Met Ile Lys Val Lys Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn
        55                                60                                65                                70
GGA TTT
Gly Phe

```

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 61..243
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 41..223
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 236..272
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 217..253
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 314..349
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 298..333
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 268..300
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 250..282
 id AA102323
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 268..434
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 211..377
 id H30432
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 147..218
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 88..159
id H30432
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 209..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 151..213
id H30432
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 250..434
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 71..255
id H08060
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 35..87
id H08060
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 449..478
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 268..297
id H08060
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 77..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 61..149
id AA088762
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 201..253
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 185..237
id AA088762
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 19..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..46
id AA088762
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..284
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 236..269
id AA088762
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 126..252
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 102..228
id HSCOWG121
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..127
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 36..102
id HSCOWG121
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 31..201
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8
seq IVRLVAFCPFASS/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

AATNGCGAGC	NGAACCCGGC	AGCTGGCGCC	ATG	GTG	CTG	TTG	CAC	GTG	CTG	TTT	54					
			Met	Val	Leu	Leu	His	Val	Leu	Phe						
											-55					
											-50					
GAG	CAC	GCG	GTC	GGC	TAC	GCG	CTG	CTG	GCG	CTG	AAG	GAA	GTG	GAG	GAG	102
Glu	His	Ala	Val	Gly	Tyr	Ala	Leu	Leu	Ala	Leu	Lys	Glu	Val	Glu	Glu	
																-45
																-40
																-35
ATC	AGT	CTG	CTG	CAG	CCG	CAG	GTG	GAG	GAG	TCC	GTG	CTC	AAC	CTG	GGC	150
Ile	Ser	Leu	Leu	Gln	Pro	Gln	Val	Glu	Glu	Ser	Val	Leu	Asn	Leu	Gly	
																-30
																-25
																-20
AAA	TTC	CAC	AGC	ATC	GTT	CGT	CTG	GTG	GCC	TTT	TGT	CCC	TTT	GCC	TCA	198
Lys	Phe	His	Ser	Ile	Val	Arg	Leu	Val	Ala	Phe	Cys	Pro	Phe	Ala	Ser	
																-15
																-10
																-5
TCC	CAG	GTT	GCC	TTG	GAA	AAT	GCC	AAC	GCC	GTG	TCT	GAA	GGG	GTT	GTT	246

Ser	Gln	Val	Ala	Leu	Glu	Asn	Ala	Asn	Ala	Val	Ser	Glu	Gly	Val	Val		
1					5					10					15		
CAT	GAG	GAC	CTC	CGC	CTG	CTC	TTG	GAG	ACC	CAC	CTG	CCG	TCC	AAA	AAG	294	
His	Glu	Asp	Leu	Arg	Leu	Leu	Leu	Glu	Thr	His	Leu	Pro	Ser	Lys	Lys		
			20					25						30			
AAG	AAA	GTA	CTC	TTG	GGA	GTT	GGG	GAT	CCC	AAG	ATT	GGT	GCC	GCA	ATA	342	
Lys	Lys	Val	Leu	Leu	Gly	Val	Gly	Asp	Pro	Lys	Ile	Gly	Ala	Ala	Ile		
			35					40					45				
CAG	GAG	GAG	TTA	GGG	TAC	AAC	TGC	CAG	ACT	GGA	GGA	GTC	ATA	GCT	GAG	390	
Gln	Glu	Glu	Leu	Gly	Tyr	Asn	Cys	Gln	Thr	Gly	Gly	Val	Ile	Ala	Glu		
			50				55					60					
ATC	CTG	CGA	RGA	GTT	CGT	CTG	CAC	TTC	CAC	AAT	CTG	GTG	AAA	GGG	TCT	438	
Ile	Leu	Arg	Xaa	Val	Arg	Leu	His	Phe	His	Asn	Leu	Val	Lys	Gly	Ser		
			65				70				75						
GAC	CGA	TGT	GKT	CAG	CTT	GTA	AAG	CAC	AGC	TGG	GGC	TGG	GAC	ACA	GCT	486	
Asp	Arg	Cys	Xaa	Gln	Leu	Val	Lys	His	Ser	Trp	Gly	Trp	Asp	Thr	Ala		
			80				85			90					95		
ATT	CCC	ATG														495	
Ile	Pro	Met															

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 20..263
id H52756
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..186
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 10..195
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 182..272
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..255
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..186
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..180
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..262
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 167..257
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..228
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 29..243
id T73900
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 83..223
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.9
seq LLLPRVLLTMASG/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```
GAAGAGGCCG CTCTTCCTGG GGTGTTTCT CCGTGTGACG TGTGGCCTTT GAGATCAACT    60
CTCCTGTACC AGCGTAGGCC GC ATG AGT GGG GGG CGG GCT CCC GCG GTC CTG    112
               Met Ser Gly Gly Arg Ala Pro Ala Val Leu
               -45                               -40
CTC GGC GGA GTG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG    160
```

```

Leu Gly Gly Val Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala
   -35                               -30                               -25

CTG CTG CCT GTG GCC TCC CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG      208
Leu Leu Pro Val Ala Ser Arg Leu Leu Leu Leu Pro Arg Val Leu Leu
   -20                               -15                               -10

ACC ATG GCC TCT GGA AGC CCT CCG ACC CAG CCC TCG CCG GCC TCG GAT      256
Thr Met Ala Ser Gly Ser Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp
   -5                               1                               5                               10

TCC GGC ATC GGG
Ser Gly Ile Gly
      15

```

268

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..177
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..164
id T09311
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 54..131
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ATGAGATCCC GGCCTCAGGG TGGACGCAGT GGTTCCTGCAC TGAGGCCCTC GTC ATG      56
                                     Met

GTG GCG CCT GTG TGG TAC TTG GTA GCG GCG GCT CTG CTA GTC GGC TTT      104
Val Ala Pro Val Trp Tyr Leu Val Ala Ala Ala Leu Leu Val Gly Phe
-25                               -20                               -15                               -10

ATC CTC TTC CTG ACT CGC AGC CGG GGC CGG GCG GCA TCA GCC GGC CAA      152
Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly Gln
      -5                               1                               5

```

GAG CCA CTG CAC AAT GAG GAG CCG GGG
Glu Pro Leu His Asn Glu Glu Pro Gly
10 15

179

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..432
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 300..403
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 70..161
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 185..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 153..246
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..77
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 275..326
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 244..295
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..88
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 275..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 240..321
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 206..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 170..242
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 314..378
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..194
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 103..156
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 37..207
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 323..432

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 259..368
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 272..326
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 207..261
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..109
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..44
id W52153
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..181
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```
ACGACGCCGG CGAGCAGTGG CCGTKACGGC CGAAAAG ATG GCG GTC TTG GCA CCT      55
                                   Met Ala Val Leu Ala Pro
                                   -45

CTA ATT GCT CTC GTG TAT TCG GTG CCG CGA CTT TCA CGA TGG CTC GCC      103
Leu Ile Ala Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala
-40                               -35                               -30

CAA CCT TAC TAC CTT CTG TCG GCC CTG CTC TCT GCT GCC TTC CTA CTC      151
Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu
-25                               -20                               -15

GTG AGG AAA CTG CCG CCG CTC TGC CAC GGT CTG CCC ACC CAA MGC GAA      199
Val Arg Lys Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Xaa Glu
-10                               -5                               1                               5

GAC GGT AAC CCG TGT GAC TTT GAC TGG AGA GAA GTG GAG ATC CTG ATG      247
Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met
10                               15                               20

TTT CTC AGT GCC ATT GTG ATG ATG AAG AAC CGC AGA TCC ATC ACT GTG      295
Phe Leu Ser Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val
25                               30                               35

GAG CAA CAT ATA GGC AAC ATT TTC ATG TTT AGT AAA GTG GCC AAC ACA      343
Glu Gln His Ile Gly Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr
40                               45                               50
```

ATT CTT TTC TTC CGC TTG GAT ATT CGC ATG GGC CTA CTT TAC ATC ACA 391
Ile Leu Phe Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr
55 60 65 70

CTC TGC ATA GTG TTC CTG ATG ACG TGC AAA CCC CCC CTT 430
Leu Cys Ile Val Phe Leu Met Thr Cys Lys Pro Pro Leu
75 80

(2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..88
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 309..390
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 240..321
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 240..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 170..242
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 382..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 314..378
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 175..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 103..156
id AA088802
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 137..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 37..207
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..453
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 259..355
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 306..360
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 207..261
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..44
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..322
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 48..300
id H15999
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..42
id H15999

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 9..215
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.6
 seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

AAGTCGTT ATG GTG GGG GAG GCG GGG CGA GAC CTA CGA CGC CGG CGA SCW      50
  Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Xaa
                -65                                -60

KTG GCC GTT ACG GCC GDD AAG ATG GCG GTC TTG GCA CCT CTA ATT GCT      98
Xaa Ala Val Thr Ala Xaa Lys Met Ala Val Leu Ala Pro Leu Ile Ala
-55                -50                -45                -40

CTC GTG TAT TCG GTG CCG CGA CTT TCA CGA TGG CTC GCC CAA CCT TAC      146
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
                -35                -30                -25

TAC CTT CTG TCG GCC CTG CTC TCT GCT GCC TTC CTA CTC GTG AGG AAA      194
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys
                -20                -15                -10

CTG CCG CCG CTC TGC CAC GGT CTG CCC ACC CAA CGC GAA GAC GGT AAC      242
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn
                -5                1                5

CCG TGT GAC TTT GAC TGG AGA GAA GTG GAG ATC CTG ATG TTT CTC AGT      290
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser
10                15                20                25

GCC ATT GTG ATG ATG AAG AAC CGC AGA TCC ATC ACT GTG GAG CAA CAT      338
Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His
                30                35                40

ATA GCC AAC ATT TTC ATG TTT AGT AAA GTG GCC AAC ACA ATT CTT TTC      386
Ile Ala Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe
                45                50                55

TTC CGC TTG GAT ATT CGC ATG GGC CTA CTT TAC ATC ACA CTC TGC ATA      434
Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile
        60                65                70

GTG TTC CTG ATG ACG TGC
Val Phe Leu Met Thr Cys
        75

```

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 236..362

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 178..304
id W69812
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 61..184

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..124
id W69812
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 359..423

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 302..366
id W69812
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 184..236

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 125..177
id W69812
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 35..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 1..361
id T09075
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 79..386

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..308
id W45253
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 386..438
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 309..361
id W45253
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..417
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..400
id AA105440
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..288
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 9..295
id H42261
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 21..164
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq LLMLLLFLSELQY/YL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```
ACCCTTTCCG GMMGGTCCCC ATG GAG GCG CTG GGG AAG CTG AAG CAG TTC GAT    53
      Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp
                        -45                                -40

GCC TAC CCC AAG ACT TTG GAG GAC TTC CGG GTC AAG ACC TGC GGG GGC    101
Ala Tyr Pro Lys Thr Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly
      -35                                -30                                -25

GCC ACC GTG ACC ATT GTC AGT GGC CTT CTC ATG CTG CTA CTG TTC CTG    149
Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu
      -20                                -15                                -10

TCC GAG CTG CAG TAT TAC CTC ACC ACG GAG GTG CAT CCT GAG CTC TAC    197
Ser Glu Leu Gln Tyr Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr
      -5                                1                                5                                10

GTG GAC AAG TCG CGG GGA GAT AAA CTG AAG ATC AAC ATC GAT GTA CTT    245
Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu
      15                                20                                25

TTT CCG CAC ATG CCT TGT GCC TAT CTG AGT ATT GAT GCC ATG GAT GTG    293
Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val
      30                                35                                40
```

GCC	GGA	GAA	CAG	CAG	CTG	GAT	GTG	GAA	CAC	AAC	CTG	TTC	AAG	CAA	CGA	341
Ala	Gly	Glu	Gln	Gln	Leu	Asp	Val	Glu	His	Asn	Leu	Phe	Lys	Gln	Arg	
45						50					55					
CTA	GAT	AAA	GAT	GGC	ATC	CCC	GTG	AGC	TCA	GAG	GCT	GAG	CGG	CAT	GAG	389
Leu	Asp	Lys	Asp	Gly	Ile	Pro	Val	Ser	Ser	Glu	Ala	Glu	Arg	His	Glu	
60					65					70					75	
CTT	GGG	AAA	GTC	GAG	GTG	ACG	GTG	TTT	GAC	CCT	GAC	TCC	CTG	GAC	CCG	437
Leu	Gly	Lys	Val	Glu	Val	Thr	Val	Phe	Asp	Pro	Asp	Ser	Leu	Asp	Pro	
				80					85						90	

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 70..161
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 304..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 300..392
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..253
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 153..246
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..84
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..77

id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 250..301
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 244..295
id AA182502
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 37..207
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 298..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 259..357
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..301
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 207..261
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..84
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..44
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 409..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 370..406
id W52153
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..103
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..88
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 250..331
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 240..321
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 181..253
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 170..242
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 323..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 314..378
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 116..169
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 103..156
id AA088802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 409..446
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 444..481
id W57342
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 13..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.6
seq FLLVRKLPPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

ACGGCCGAAA AG ATG GCG GTC TTG GCA CCT CTA ATT GCT CTC GTG TAT TCG 51

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser
-45 -40

GTG CCG CGA CTT TCA CGA TGG CTC GCC CAA CCT TAC TAC CTT CTG TCG	99
Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser	
-35 -30 -25 -20	
GCC CTG CTC TCT GCT GCC TTC CTA CTC GTG AGG AAA CTG CCG CCG CTC	147
Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu	
-15 -10 -5	
TGC CAC GGT CTG CCC ACC CAA CGC GAA GAC GGT AAC CNN TGT GAC TTT	195
Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe	
1 5 10	
GAC TGG AGA GAA GTG GAG ATC CTG ATG TTT CTC AGT GCC ATT GTG ATG	243
Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met	
15 20 25	
ATG AAG AAC CGC AGA TCC ATC ACT GTG GAG CAA CAT ATA GGC AAC ATT	291
Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile	
30 35 40 45	
TTC ATG TTT AGT AAA GTG GCC AAC ACA ATT CTT TTC TTC CGC TTG GAT	339
Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp	
50 55 60	
ATT CGC ATG GGC CTA CTT TRC ATC ACA CTC TGC ATA GTG TTC CTG ATG	387
Ile Arg Met Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met	
65 70 75	
ACG TGC AAA CCC CCC CTA TAT ATG GGC CCT GAG TAT ATC AVG TAC TTC	435
Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe	
80 85 90	
AAT GAT AAA	444
Asn Asp Lys	
95	

(2) INFORMATION FOR SEQ ID NO: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..272

id C18312
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 259..385
id C18312
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 87..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 59..265
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 252..339
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 22..68
id R99140
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 92..252
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 281..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 239..314
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..94
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 25..55
id T78951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..132
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 62..92
id T78951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 133..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 144..305
id W69247
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 280..332
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 292..344
id W69247
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 49..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 62..108
id W69247
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 97..308
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 69..280
id H75891
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..69
id H75891
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 306..335
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 280..309
 id H75891
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 55..111
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.4
 seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

AGCCTCCCGA TTGACTGGCC TGCTTGCAA BGCAAGTAGC GCGGCGCTT CAAG ATG	57
Met	
CGC TGC CTG ACC ACG CCT ATG CTG CTG CGG GCC CTG GCC CAG GCT GCA	105
Arg Cys Leu Thr Thr Pro Met Leu Arg Ala Leu Ala Gln Ala Ala	
-15 -10 -5	
CGT GCA GGA CCT CCT GGT GGC CGG AGC CTC CAC AGC AGT GCA GTG GCA	153
Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val Ala	
1 5 10	
GCC ACC TAC AAG TAT GTG AAC ATG CAG GAT CCC GAG ATG GAC ATG AAG	201
Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met Lys	
15 20 25 30	
TCA GTG ACT GAC CGG GCA GCC CGC ACC CTG CTG TGG ACT GAG CTC TTC	249
Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu Phe	
35 40 45	
CGA GGC CTG GGC ATG ACC CTG AGC TAC CTG TTC CGG GAA CCG GCC ACC	297
Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala Thr	
50 55 60	
ATC AAC TAC CCG TTC GAG AAG GGC CCG CTG AGC CCT CGC TTC CGT GGG	345
Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg Gly	
65 70 75	
GAG CAT GCG CTG CGC CGG TAC CCA TCC GGG GAG GAG CGT TGC ATT GCC	393
Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile Ala	
80 85 90	
TGC AAG CTC TGC	405
Cys Lys Leu Cys	
95	

(2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 415 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE ..
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 2..261

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 13..272
id C18312
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 249..415

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 259..425
id C18312
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 55..261

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 59..265
id R99140
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 17..63

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 22..63
id R99140
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 101..261

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 92..252
id T78951
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 249..324

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 239..314
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 62..92
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..62
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 25..55
id T78951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..277
id C16677
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 69..280
id H75891
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..63
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 8..69
id H75891
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 280..309
id H75891
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 23..79
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```

AAAGTAGCGG CGGCGCTTCA AG ATG CGC TGC CTG ACC ACG CCT ATG CTG CTG      52
                        Met Arg Cys Leu Thr Thr Pro Met Leu Leu
                        -15                                -10

CGG GCC CTG GCC CAG GCT GCA CGT GCA GGA CCT CCT GGT GGC CGG AGC      100
Arg Ala Leu Ala Gln Ala Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser
                        -5                                1                                5

CTC CAC AGC AGT GCA GTG GCA GCC ACC TAC AAG TAT GTG AAC ATG CAG      148
Leu His Ser Ser Ala Val Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln
                        10                                15                                20

GAT CCC GAG ATG GAC ATG AAG TCA GTG ACT GAC CGG GCA GCC CGC ACC      196
Asp Pro Glu Met Asp Met Lys Ser Val Thr Asp Arg Ala Ala Arg Thr
                        25                                30                                35

CTG CTG TGG ACT GAG CTC TTC CGA GGC CTG GGC ATG ACC CTG AGC TAC      244
Leu Leu Trp Thr Glu Leu Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr
                        40                                45                                50                                55

CTG TTC CGG GAA CCG NCC ACC ATC AAC TAC CCG TTC GAG AAG GGC CCG      292
Leu Phe Arg Glu Pro Xaa Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro
                        60                                65                                70

CTG AGC CCT CGC TTC CGT GGG GAG CAT GCG CTG CGC CGG TAC CCA TCC      340
Leu Ser Pro Arg Phe Arg Gly Glu His Ala Leu Arg Arg Tyr Pro Ser
                        75                                80                                85

GGG GAG GAG CGT TGC ATT GCC TGC AAG CTC TGC GAG GCC ATC TGC CCC      388
Gly Glu Glu Arg Cys Ile Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro
                        90                                95                                100

GCC CAG GCC ATC ACC ATC GAG GCT GAG      415
Ala Gln Ala Ile Thr Ile Glu Ala Glu
                        105                                110

```

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..349

id N40260
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 351..402
id N40260
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 22..369
id W37568
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..297
id AA135041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 335..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 297..358
id AA135041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 114..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 74..260
id W00732
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 263..347
id W00732
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..284
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 16..299
id W07706
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 285..323
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 301..339
id W07706
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..121
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq ILPLLFGLGVFG/LF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```

GAAGTTGCTT GACTATGGTC TCTCCGGCTA CCAGGAAGAG TCTGCCGAAG TGAAGGCC      58
ATG GAC TTC ATC ACC TCC ACA GCC ATC CTG CCC CTG CTG TTC GGC TGC      106
Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
-20                               -15                               -10

CTG GGC GTC TTC GGC CTC TTC CGG CTG CTG CAG TGG GTG CGC GGG AAG      154
Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5                               1                               5                               10

GCC TAC CTG CGG AAT GCT GTG GTG GTG ATC ACA GGC GCC ACC TCA GGG      202
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
15                               20                               25

CTG GGC AAA GAA TGT GCA AAA GTC TTC TAT GCT GCG GGT GCT AAA CTG      250
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
30                               35                               40

GTG CTC TGT GGC CGG AAT GGT GGG GCC CTA GAA GAG CTC ATC AGA GAA      298
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45                               50                               55

CTC ACC GCT TCT CAT GCC ACC AAG GTG CAG ACA CAC AAG CCT TAC TTG      346
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
60                               65                               70                               75

GTA CKN TTN GAC CTC ACA GAC TCT GGG GCC ATA GTT GCA GCA GCA GCT      394
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
80                               85                               90

GAG ATC TGC AGT
Glu Ile Cys Ser
95

```

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Lymph ganglia
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 18..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..281
 id C17369
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 18..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..281
 id HUM522E11B
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 42..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..257
 id HUM503D01B
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 82..298
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 46..262
 id N30487
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 35..70
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..36
 id N30487
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 19..252

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..234
id C17067
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 162..248
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq LLLVTWVFTPVT/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
AGTGTTCGCC GCTGGAGCCC GGGTCGAGAG GACGAGGTGC CGCTGCCTGG AGAATCCTCC   60
GCTGCCGTCTG GCTCCCGGAG CCCAGCCCTT TCCTAACCCA ACCCAACCTA GCCCAGTCCC   120
AGCCGMCAGM GCCTGTCCCT RTCACGGACC CCAGCGTTAC C ATG CAT CCT GCC GTC   176
                                         Met His Pro Ala Val
                                         -25

TTC CTA TCC TTA CCC GAC CTC AGA TGC TCC CTT CTG CTC CTG GTA ACT   224
Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser Leu Leu Leu Leu Val Thr
          -20                      -15                      -10

TGG GTT TTT ACT CCT GTA ACA ACT GAA ATA ACA AGT CTT GAT ACA GAG   272
Trp Val Phe Thr Pro Val Thr Thr Glu Ile Thr Ser Leu Asp Thr Glu
          -5                      1                      5

VGT ATA GAT GAA ATT TTA AAC AAT GCA TTG   302
Xaa Ile Asp Glu Ile Leu Asn Asn Ala Leu
      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 76..259
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 97.3
region 1..184
id HSU72245
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 73..178
id W25639
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 179..270
id W25639
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 38..82
id W25639
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 11..258
id R72515
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..228
id AA040016
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..223
id T84313
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..227
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 129..286
id H57207

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 225..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 285..319
id H57207
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 76..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
AAAGTGCTCA GCCCCCGGGG SACAGCAGGA CGTTTGGGGG CCTTCTTTCA GCAGGGGACA      60
GCCCGATTGG GGACA ATG GCG TCT CTT GGC CAC ATC TTG GTT TTC TGT GTG      111
          Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val
          -20                      -15                      -10

GGT CTC CTC ACC ATG GCC AAG GCA GAA AGT CCA AAG GAA CAC GAC CCG      159
Gly Leu Leu Thr Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro
          -5                      1                      5

TTC ACT TAC GAC TAC CAG TCC CTG CAG ATC GGA GGC CTC GTC ATC GCC      207
Phe Thr Tyr Asp Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala
          10                      15                      20

GGG ATC CTC TTC ATC CTG GGC ATC CTC ATC GTG CTG AGC AGA AGA TGC      255
Gly Ile Leu Phe Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys
          25                      30                      35                      40

CGG TTT CGG      264
Arg Phe Arg
```

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..444

(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 91.9
region 164..604
id RNGP55
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..444
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 90.6
region 567..901
id RNGP56
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..444
(C) IDENTIFICATION METHOD: fasta
(D) OTHER INFORMATION: identity 91.4
region 1..439
id D50463
vrt

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 205..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 300..393
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 120..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 214..299
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 95..156
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 56..119
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 149..212
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 297..340
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 393..436
id AA173361
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..339
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..321
id R14826
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 345..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 330..362
id R14826
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..444
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 133..408
id W75505
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..171
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 1..138
id W75505
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..246
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 165..352
id AA206770
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 284..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 393..460
id AA206770
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 1..69
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 91
 region 105..173
 id AA206770
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 243..286
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 351..394
 id AA206770
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 169..415
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 133..379
 id W64115
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 34..171
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 1..138
 id W64115
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 30..98
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.3
 seq ALSLLLVSGLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```

ATTCGCTGTT GGGTCTTCTG CTAGGGAGG ATG TCG GGT TCG TCG CTG CCC AGC      53
                               Met Ser Gly Ser Ser Leu Pro Ser
                               -20

GCC CTG GCC CTC TCG CTG TTG CTG GTC TCT GGC TCC CTC CTC CCA GGG      101
Ala Leu Ala Leu Ser Leu Leu Leu Val Ser Gly Ser Leu Leu Pro Gly
-15                               -10                               -5                               1

CCA GGC GCC GGT CAG AAC GAG CCA AGG ATT GTC ACC AGT GAA GAG GTC      149
Pro Gly Ala Ala Gln Asn Glu Pro Arg Ile Val Thr Ser Glu Glu Val
          5                               10                               15

ATT ATT CGA GAC AGC CCT GTT CTC CCT GTC ACC CTG CAG TGT AAC CTC      197
Ile Ile Arg Asp Ser Pro Val Leu Pro Val Thr Leu Gln Cys Asn Leu

```

	20	25	30	
ACC TCC AGC TCT CAC ACC CTT ACA TAC AGC TAC TGG ACA AAG AAT GGG				245
Thr Ser Ser Ser His Thr Leu Thr Tyr Ser Tyr Trp Thr Lys Asn Gly				
35		40	45	
GTG GAA CTG AGT GCC ACT CGT AAG AAT GCC AGC AAC ATG GAG TAC AGG				293
Val Glu Leu Ser Ala Thr Arg Lys Asn Ala Ser Asn Met Glu Tyr Arg				
50	55	60	65	
ATC AAT AAG CCG AGA GCT GAG GAT TCA GGC GAA TAC CAC TGC GTA TAT				341
Ile Asn Lys Pro Arg Ala Glu Asp Ser Gly Glu Tyr His Cys Val Tyr				
	70	75	80	
CAC TTT GTC AGC GCT CCT AAA GCA AAC GCC ACC ATT GAA GTG AAA GCC				389
His Phe Val Ser Ala Pro Lys Ala Asn Ala Thr Ile Glu Val Lys Ala				
	85	90	95	
GCT CCT GAC ATC ACT GGC CAT AAA CGG AGT DAG AAC AAG AAT GAA GGG				437
Ala Pro Asp Ile Thr Gly His Lys Arg Ser Xaa Asn Lys Asn Glu Gly				
100	105	110		
CAG GAT				443
Gln Asp				
115				

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..130
id AA056148
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..358
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 369..480
id AA056148
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..251
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 261..372
id AA056148
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 227..313
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 24..94
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 216..271
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 304..359
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 294..342
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 384..432
id AA134519
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..426
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 6..292
id HUM1495063
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 150..426
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..331
id AA187561
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 140..423
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 77..360
 id W51338
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 137..244
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.2
 seq IMLLSLAAFSVIS/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

AGTCTGTCGG ASTCTGTCCT CGGAGCAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC      60
CGGATTATTC TATTTCCCTT CCCTCTCTSC CGCCCCGTAT CTCTTTTCAC CTTTCTCCCA    120
CCCTCGCTCG CGTRSC ATG GCG GTG CAC GAT CTG ATT TTC TGG AGA GAT GTG      172
           Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val
           -35                               -30                       -25

AAG AAG ACT GGG TTT GTC TTT GGC ACC ACG CTG ATC ATG CTG CTT TCC      220
Lys Lys Thr Gly Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser
           -20                               -15                       -10

CTG GCA GCT TTC AGT GTC ATC AGT GTG GTT TCT TAC CTC ATC CTG GCT      268
Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr Leu Ile Leu Ala
           -5                               1                               5

CTT CTC TCT GTC ACC ATC AGC TTC AGG ATC TAC AAG TCC GTC ATC CAA      316
Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val Ile Gln
           10                               15                               20

GCT GTA CAG AAG TCA GAA GAA GGC CAT CCA TTC AAA GCC TAC CTG GAC      364
Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys Ala Tyr Leu Asp
           25                               30                               35                       40

GTA GAC ATT ACT CTG TCC TCA GAA GCT TTC CAT AAT TAC ATG AAT GCT      412
Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala
           45                               50                               55

GCS ATG GTG CAC
Ala Met Val His
           60

```

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 194..260

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 171..237
id AA213022
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 35..130

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.1
seq LLWTL LLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```
CTGGCACCTC TTCCGTCGGC TGAATTGCGG CCGT ATG CRC GGC TCT GTG GAG TGC      55
                               Met Xaa Gly Ser Val Glu Cys
                               -30

ACC TRG GGT TGG GGG CAC TGT GCC CCC AGC CCC CTG CTC CTT TGG ACT      103
Thr Xaa Gly Trp Gly His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr
-25                               -20                               -15                               -10

CTA CTT CTG TTT GCA GCC CCA TTT GGC CTG CTG GGG GAG AAG ACC CGC      151
Leu Leu Leu Phe Ala Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr Arg
                               -5                               1                               5

CAG GTG TCT CTG GAG GTC ATC CCT AAC TGG CTG GGC CCC CTG CAG AAC      199
Gln Val Ser Leu Glu Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn
                               10                               15                               20

CTG CTT CAT ATA CGG GCA GTG GGC ACC AAT TCC ACA CTG CAC TAT GTG      247
Leu Leu His Ile Arg Ala Val Gly Thr Asn Ser Thr Leu His Tyr Val
                               25                               30                               35

TGG AGC AGC CTG GGG CCT CTG GCA GTG GTA ATG GTG GCC ACC AAC ACC      295
Trp Ser Ser Leu Gly Pro Leu Ala Val Val Met Val Ala Thr Asn Thr
                               40                               45                               50                               55

CCC CCC GGG
Pro Pro Gly
304
```

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 47..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 30..314
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 330..429

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 314..413
id AA100852
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 47..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 30..314
id AA161042
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 338..422

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 323..407
id AA161042
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 23..335

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 1..313
id H64488
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..366

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 129..354
id AA088770
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..121
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 17..106
id AA088770
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 116..317
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 134..335
id AA146605
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 317..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 336..397
id AA146605
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 137..223
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.1
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```
AAGTGGTGTG TGAGAGCCAG GCGTCCCTCT GCCTGCCCAC TCAGTGGCAA CACCCGGGAG    60
CTGTTTTGTC CTTTGTGGAG CCTCAGCAGT TCCCTCTTTC AGAACTCACT GCCAAGAGCC    120
CTGAACAGGA GCCACC ATG CAG TGC TTC AGC TTC ATT AAG ACC ATG ATG ATC    172
      Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile
                        -25                        -20

CTC TTC AAT TTG CTC ATC TTT CTG TGT GGT GCA GCC CTG TTG GCA GTG    220
Leu Phe Asn Leu Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val
      -15                        -10                        -5

GGC ATC TGG GTG TCA ATC GAT GGG GCA TCC TTT CTG AAG ATC TTC GGG    268
Gly Ile Trp Val Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly
      1                        5                        10                        15

CCA CTG TCG TCC AGT GCC ATG CAG TTT GTC AAC GTG GGC TAC TTC CTC    316
Pro Leu Ser Ser Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu
      20                        25                        30

ATC GCA GCC GGC GTT GTG GTC TTT GCT CTT GGT TTC CTG GGC TGC WMT    364
Ile Ala Ala Gly Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa
      35                        40                        45
```

GGT GCT AAG RCT GAG ARC AAG TGT GCC CTC GTG ACG TTC TTC TTC ATC	412
Gly Ala Lys Xaa Glu Xaa Lys Cys Ala Leu Val Thr Phe Phe Phe Ile	
50 55 60	
CTC CTC CTC ATC TTC	427
Leu Leu Leu Ile Phe	
65	

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 18..111
id N28008
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 108..152
id N28008
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 16..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLWTLLLF AAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AAGAATTGCG GCCGT ATG CGC GGC TCT GTG GAG TGC ACC TGG GGT TSG GGG	51
Met Arg Gly Ser Val Glu Cys Thr Trp Gly Xaa Gly	
-30 -25	
CAC TGT GCC CCC AGC CCC CTG CTC CTT TGG ACT CTA CTT CTG TTT GCA	99
His Cys Ala Pro Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala	
-20 -15 -10 -5	

GCC CCA TTT GGC CTG CTG GGG GAG AAG ACC CAC CAG GTG TCT CTG GAG	147
Ala Pro Phe Gly Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu	
1 5 10	
GTC ATC CCT AAC TGG CTG GGC CCC CTG CAG AAC CTG CTT CAT ATA CGG	195
Val Ile Pro Asn Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg	
15 20 25	
BCA GTG GGC ACC AAT TCC ACA CTG CAC TAT GTG TGG AGC AGC CTG GGG	243
Xaa Val Gly Thr Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly	
30 35 40	
CCT CTG GCA GTG GTA ATG GTG GCC ACC AAC ACC CCC CAC AGC ACC CTG	291
Pro Leu Ala Val Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu	
45 50 55 60	
AGC GTC AAC TGG AGC CTC CTG CTA TCC CCT GAG CCC GAT GGG GGC CTG	339
Ser Val Asn Trp Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu	
65 70 75	
ATG GTG CTC CCT AAG GAC AGC ATT CAG TTT TCT TCT	375
Met Val Leu Pro Lys Asp Ser Ile Gln Phe Ser Ser	
80 85	

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 164..234
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 163..233
id AA113990
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 46..103
id AA113990
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..44

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..50
id AA113990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..140
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 113..142
id AA113990
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 71..202
id R11825
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..98
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..68
id R11825
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 83..205
id H08475
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 27..98
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..72
id H08475
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 175..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 142..201
id C14102
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..103
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 25..68
id C14102
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 136..234
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..99
id N87606
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..82
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7
seq LRLKLAATSASA/RV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```
ACCCTTGGGT CCTTGATCCT GAGCTGACCG GGTAGCC ATG GCC TTG CGG CTC CTG      55
                               Met Ala Leu Arg Leu Leu
                               -15                               -10

AAG CTG GCA GCG ACG TCC GCG TCC GCC CGG GTC GTG GCG GCG GGC GCC      103
Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg Val Val Ala Ala Gly Ala
               -5                               1                               5

CAG CGC GTG AGA GGA ATT CAT AGC AGT GTG CAG TGC AAG CTG CGC TAT      151
Gln Arg Val Arg Gly Ile His Ser Ser Val Gln Cys Lys Leu Arg Tyr
               10                               15                               20

GGA ATG TGG CAT TTC CTA CTT GGG GAT AAA GCA AGC AAA AGA CTG ACA      199
Gly Met Trp His Phe Leu Leu Gly Asp Lys Ala Ser Lys Arg Leu Thr
               25                               30                               35

GAA CGC AGC AGA GTG ATA ACT GTA GAT GGC AAT ATG                      235
Glu Arg Ser Arg Val Ile Thr Val Asp Gly Asn Met
               40                               45                               50
```

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 409 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..399
id AA233701
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..62
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 7..50
id AA233701
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 148..409
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 106..367
id N39913
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..108
id N39913
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 42..169
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 39..166
id HUM527C01B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..284
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 165..280
id HUM527C01B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..42
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100

region 1..38
id HUM527C01B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..118
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..107
id AA280711
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 62..256
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7
seq IGHFLCLVILVYC/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```
CTCTGTGGAT TCTGGCCAGG CCGGGTTCGG CGGTTGCTGT GAGAGCGGGC TTCCCAACAC      60
C ATG CCG TCC GCC TTC TCT GTC AGC TCT TTC CCC GTC AGC ATC CCA GCC      109
  Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
  -65                -60                -55                -50

GTG CTC ACG CAG ACG GAC TGG ACT GAG CCC TGG CTC ATG GGG CTG GCC      157
Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
                -45                -40                -35

ACC TTC CAC GCG CTC TGC GTG CTC CTC ACC TGC TTG TCC TCC CGA AGC      205
Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
                -30                -25                -20

TAC AGA CTA CAG ATC GGG CAC TTT CTG TGT CTA GTC ATC TTA GTC TAC      253
Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
                -15                -10                -5

TGT GCT GAA TAC ATC AAT GAG GCG GCT GCG ATG AAC TGG AGA TTA TTT      301
Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
    1                5                10                15

TCG AAA TAC CAG TAT TTC GAC TCC AGG GGG ATG TTC ATT TCT ATA GTA      349
Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
                20                25                30

TTT TCA GCC CCA CTG CTG GTG AAT GCC ATG ATC ATT GTG GTT ATG TGG      397
Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
                35                40                45

GTA TGG AAG ACT                                          409
Val Trp Lys Thr
    50
```

(x) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 192..336
id T53942
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 88..223
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 59..194
id T53942
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..88
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..58
id T53942
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 345..383
id T53942
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 47..364
id R55646
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..35
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 18..51
id R55646
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 47..238
id H21573
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 220..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 236..341
id H21573
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..35
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 18..51
id H21573
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..296
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 2..254
id W47454
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 265..304
id W47454
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 395..426
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 360..391
id W47454
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 39..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 36..220
id T71932
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 220..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 218..270
id T71932
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 4..37
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 2..35
id T71932
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 26..487
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq ALGILVVAGCSFA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

AAHCAGACCT CCTCTTGGCT TCGAG ATG GCT TTG CCA CAC CAA GAG CCC AAA	52
Met Ala Leu Pro His Gln Glu Pro Lys	
-150	
CCT GGA GAC CTG ATT GAG ATT TTC CGC CTT GGC TAT GAG CAC TGG GCC	100
Pro Gly Asp Leu Ile Glu Ile Phe Arg Leu Gly Tyr Glu His Trp Ala	
-145 -140 -135 -130	
CTG TAT ATA BGA GAT GGC TAC GTG ATC CAT CTG GCT CCT CCA AGT GAG	148
Leu Tyr Ile Xaa Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu	
-125 -120 -115	
TAC CCC GGG GCT GGC TCC TCC AGT GTC TTC TCA GTC CTG AGC AAC AGT	196
Tyr Pro Gly Ala Gly Ser Ser Ser Val Phe Ser Val Leu Ser Asn Ser	
-110 -105 -100	
GCA GAG GTG AAA CGG GAG CGC CTG GAA GAT GTG GTG GGA GGC TGT TGC	244
Ala Glu Val Lys Arg Glu Arg Leu Glu Asp Val Val Gly Gly Cys Cys	
-95 -90 -85	
TAT CGG GTC AAC AAC AGC TTG GAC CAT GAG TAC CAA CCA CGG CCC GTG	292
Tyr Arg Val Asn Asn Ser Leu Asp His Glu Tyr Gln Pro Arg Pro Val	
-80 -75 -70	
GAG GTG ATC ATC AGT TCT GCG AAG GAG ATG GTT GGT CAG AAG ATG AAG	340
Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys	

-65	-60	-55	-50	
TAC AGT ATT GTG AGC AGG AAC TGT GAG CAC TTT GTC ACC CAG CTG AGA				388
Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg				
	-45	-40	-35	
TAT GGC AAG TCC CGC TGT AAA CAG GTG GAA AAG GCC AAG GTT GAA GTC				436
Tyr Gly Lys Ser Arg Cys Lys Gln Val Glu Lys Ala Lys Val Glu Val				
	-30	-25	-20	
GGT GTG GCC ACG GCG CTT GGA ATC CTG GTT GTT GCT GGA TGC TCT TTT				484
Gly Val Ala Thr Ala Leu Gly Ile Leu Val Val Ala Gly Cys Ser Phe				
	-15	-10	-5	
GCG ATT AGG AGA TAC CAA AAA AAA GCG ACC				514
Ala Ile Arg Arg Tyr Gln Lys Lys Ala Thr				
1	5			

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..119
id AA114211
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 177..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 143..225
id AA114211
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 30..118
id AA121286
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 214..287
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 177..250
 id AA121286
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 276..340
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 238..302
 id AA121286
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 35..64
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..30
 id AA121286
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 13..222
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LAFSLPALPLAEL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

AGAGTCGGGA AA ATG GCT GCG AGT ACC TCC ATG GTC CCG GTG GCT GTG ACG      51
    Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr
        -70                      -60

GCG GCA GTG GCG CCT GTC CTG TCC ATA AAC AGC GAT TTC TCA GAT TTG      99
Ala Ala Val Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu
    -55                      -50                      -45

CGG GAA ATT AAA AAG CAA CTG CTG CTT ATT GCG GGC CTT ACC CGG GAG     147
Arg Glu Ile Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu
    -40                      -35                      -30

CGG GGC CTA CTA CAC AGT AGC AAA TGG TCG GCG GAG TTG GCT TTC TCT     195
Arg Gly Leu Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser
    -25                      -20                      -15                      -10

CTC CCT GCA TTG CCT CTG GCC GAG CTG CAA CCG CCT CCG CCT ATT ACA     243
Leu Pro Ala Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr
        -5                      1                      5

GAG GAA GAT GCC CAG GAT ATG GAT GCC TAT ACC CTG GCC AAG GCC TAC     291
Glu Glu Asp Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr
    10                      15                      20

```

TTT	GAC	GTT	AAA	GAG	TAT	GAT	CGG	GCA	GCA	CAT	TTC	CTG	CAT	GGC	TGC	339
Phe	Asp	Val	Lys	Glu	Tyr	Asp	Arg	Ala	Ala	His	Phe	Leu	His	Gly	Cys	
25						30					35					
AAT	GCA	AGA	WAA	GCC	TAT	TTT	CTG	TAT	ATG	TAT	TCC	AGA	TAT	CTG	TCT	387
Asn	Ala	Arg	Xaa	Ala	Tyr	Phe	Leu	Tyr	Met	Tyr	Ser	Arg	Tyr	Leu	Ser	
40					45				50					55		

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 116..333
id H42954
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..117
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..111
id H42954
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..388
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 332..381
id H42954
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..436
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 275..404
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..224
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 94..194
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..89
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 191..288
id N36051
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..117
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..111
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..319
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 197..294
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 144..223
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 120..199
id N33866
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 307..349
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 281..323
id N33866
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 346..382
id N33866
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 65..165
id N79656
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 162..259
id N79656
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..117
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..60
id N79656
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 367..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 307..346
id N79656
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 86..291
id HUM424A03B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..117
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..81

id HUM424A03B
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 154..225
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq KMVHLLVLSGAWG/MQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```

AAAACCCACG AGGGGACGCG GCCGAGGAGG GTCGCTGTCC ACCCGGGGGC GTGGGAGTGA 60
GGTACCAGAT TCAGCCCATT TGGCCCCGAC GCCTCTGTTC TCGGAATCCG GGTGCTKCGC 120
GATTNRAGGT CCCGGTTCCT AACGGACTGC AAG ATG GAG GAA GGC GGG AAC CTA 174
Met Glu Glu Gly Gly Asn Leu
-20

GGA GGC CTG ATT AAG ATG GTC CAT CTA CTG GTC TTG TCA GGT GCC TGG 222
Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp
-15 -10 -5

GGC ATG CAA ATG TGG GTG ACC TTC GTC TCA GGC TTC CTG CTT TTC CGA 270
Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg
1 5 10 15

AGC CTT CCC CGA CAT ACC TTC GGA CTA GTG CAG AGC AAA CTC TTC CCC 318
Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro
20 25 30

TTC TAC TTC CAC ATC TCC ATG GGC TGT GCC TTC ATC AAY NTC TGC ATC 366
Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Xaa Cys Ile
35 40 45

TTG GCT TCA CAG CAT GCT TGG GCT CAG CTC ACA TTC TGG GAG GCC AGC 414
Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser
50 55 60

CAG CTT TAC CTG CTG TTC CTG 435
Gln Leu Tyr Leu Leu Phe Leu
65 70

```

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..269
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 151..247
id W04736
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..49
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..33
id W04736
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 44..200
id HUM054D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..110
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 6..52
id HUM054D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 6..218
id HUM065G09B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..217
id HUM062A01B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..110
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 5..52

id HUM062A01B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..191
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 10..135
id HUM048E08B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 179..276
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 124..221
id HUM048E08B
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 14..256
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq LLLASGTTLFCTS/FY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

ATGTTCTACA GCT ATG GCC GGG CCA GCT GCA GCT TTC CGC CGC TTG GGC	49
Met Ala Gly Pro Ala Ala Ala Phe Arg Arg Leu Gly	
-80 -75 -70	
GCC TTG TCC GGA GCT GCG GCC TTA GGC TTC GCT TCC TAC GGG GCG CAC	97
Ala Leu Ser Gly Ala Ala Ala Leu Gly Phe Ala Ser Tyr Gly Ala His	
-65 -60 -55	
GGC GCC BAA TTC CCA GAT GCC TAC GGG AAG GAG CTG TTT GAC AAG GCC	145
Gly Ala Xaa Phe Pro Asp Ala Tyr Gly Lys Glu Leu Phe Asp Lys Ala	
-50 -45 -40	
AAC AAA CAC CAC TTC TTA CAC AGC CTG GCC CTG TTA GGG GTG CCC CAT	193
Asn Lys His His Phe Leu His Ser Leu Ala Leu Leu Gly Val Pro His	
-35 -30 -25	
TGC AGA AAG CCA CTC TGG GCT GGG TTA TTG CTA GCT TCC GGA ACG ACC	241
Cys Arg Lys Pro Leu Trp Ala Gly Leu Leu Leu Ala Ser Gly Thr Thr	
-20 -15 -10	
TTA TTC TGC ACC AGC TTT TAC TAC CAG GCT CAG	274
Leu Phe Cys Thr Ser Phe Tyr Tyr Gln Ala Gln	
-5 1 5	

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..143
id H06750
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 14..127
id R09748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..181
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..76
id AA025704
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 45..107
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.5
seq LLTLLLPPPPPLYT/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

ACTCTTCCGG GTCGGCGCTC CTGCCTCCCT GCAGGGAGCT GCTT ATG GGA CAC CGC	56
Met Gly His Arg	
-20	
TTC CTG CGC GGC CTC TTA ACG CTG CTG CTG CCG CCG CCA CCC CTG TAT	104
Phe Leu Arg Gly Leu Leu Thr Leu Leu Leu Pro Pro Pro Pro Leu Tyr	
-15 -10 -5	
ACC CGG CAC CGC ATG CTC GGT CCA GAG TCC GTC CCG CCC CCA AAA CGA	152
Thr Arg His Arg Met Leu Gly Pro Glu Ser Val Pro Pro Pro Lys Arg	
1 5 10 15	
TCC CGC AGC AAA CTC ATG GCA CCG CCC CGG	182
Ser Arg Ser Lys Leu Met Ala Pro Pro Arg	

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 48..320
id AA081335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..80
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..49
id AA081335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 205..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 82..229
id H88204
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 121..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..98
id H88204
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..160

id W31695
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 111..170
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.5
seq ILFLLPSICSSNS/TG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```

AACATTCACT ASRCCTTTTC CATTGCTAA TAAGGCCCTG CCAGGCTGGG AGGGAATTGT      60
CCCTGCCTGC TTCTGGAGMA MAGAAGATAT TGACACCATC TACGGGCACC ATG GAA      116
                                         Met Glu
                                         -20

CTG CTT CAA GTG ACC ATT CTT TTT CTT CTG CCC AGT ATT TGC AGC AGT      164
Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys Ser Ser
-15                               -10                               -5

AAC AGC ACA GGT GTT TTA GAG GCA GCT AAT AAT TCA CTT GTT GTT ACT      212
Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val Val Thr
1                               5                               10

ACA ACA AAW CCA TCT ATA ACA ACA CCA AAC ACA GAA TCA TTA CAG AAA      260
Thr Thr Xaa Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu Gln Lys
15                               20                               25                               30

AAT GTT GTC ACA CCA ACA ACT GGA ACA ACT CHT AAA GGA ACA ATC ACC      308
Asn Val Val Thr Pro Thr Thr Gly Thr Thr Xaa Lys Gly Thr Ile Thr
35                               40                               45

AAT GAA TTA CTT AAA ATG TCT CTG ATG TCA ACA GCT VCT TTT      350
Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Xaa Phe
50                               55                               60

```

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..372
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 33..329

id H97426
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 369..413
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 327..371
id H97426
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..238
id W44834
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..120
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 4..54
id R57989
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..154
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 62..91
id R57989
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 112..168
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLMRLVASAYSIA/QK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

```
TTTGACAGTG CCAMAGCTCG GTACTGGACA CAACGAGGGA CCTGGGTCTA CGATAACGCG      60
CTTTTGCTCC TCCTGAAGTG TCTTTGGTCC AACGTTGTTC CAGASTGTAC C ATG GCT      117
                               Met Ala

TCC AGT AAC ACT GTG TTG ATG CGG TTG GTA GCC TCC GCA TAT TCT ATT      165
Ser Ser Asn Thr Val Leu Met Arg Leu Val Ala Ser Ala Tyr Ser Ile
      -15                               -10                               -5

GCT CAA AAG GCA GGA ATG ATA GTC AGA CGT GTT ATT GCT GAA GGA GAC      213
Ala Gln Lys Ala Gly Met Ile Val Arg Arg Val Ile Ala Glu Gly Asp
      1                               5                               10                               15
```

CTG GGT ATT GTG GAG AAG ACC TGT GCA ACA GAC CTG CAG ACC AAA GCT	261
Leu Gly Ile Val Glu Lys Thr Cys Ala Thr Asp Leu Gln Thr Lys Ala	
20 25 30	
GAC CGA TTG GCA CAG ATG AGC ATA TGT TCT TCA TTG GCC CGG AAA TTC	309
Asp Arg Leu Ala Gln Met Ser Ile Cys Ser Ser Leu Ala Arg Lys Phe	
35 40 45	
CCC AAA CTC ACA ATT ATA GGG GAA GAG GAT CTG CCT TCT GAG GAA GTG	357
Pro Lys Leu Thr Ile Ile Gly Glu Glu Asp Leu Pro Ser Glu Glu Val	
50 55 60	
GAT CAA GAG CTG ATT GAA GAC AGT CAG TGG GAA GAA ATA CTG AAG CAA	405
Asp Gln Glu Leu Ile Glu Asp Ser Gln Trp Glu Glu Ile Leu Lys Gln	
65 70 75	
CCA TGC CCA TCG CAG TAC AGT GCT ATT AAA GAA GAA GAT CTC GTG GTC	453
Pro Cys Pro Ser Gln Tyr Ser Ala Ile Lys Glu Glu Asp Leu Val Val	
80 85 90 95	
TGG GTT GAT	462
Trp Val Asp	

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..267
id HSU46357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 291..333
id HSU46357
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 84..128

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 6.3

seq SSCVLLTALVALA/AY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```

GCGGGCAGAA AGTTGCCGGA GGTCTCCGGG TGGTATCGCC CTTTCCTCTT TGCCAGCCCCG    60
CTGGCGAGCC GAGCCGGGGC AAG ATG AGG TCG TCC TGT GTC CTG CTC ACC GCC    113
      Met Arg Ser Ser Cys Val Leu Leu Thr Ala
      -15                               -10

CTG GTG GCG CTG GCC GCC TAT TAC GTC TAC ATC CCG CTG CGT GGC TCC    161
Leu Val Ala Leu Ala Ala Tyr Tyr Val Tyr Ile Pro Leu Pro Gly Ser
  -5                               1                               5                               10

GTG TCC GAC CCC TGG AAG CTG ATG CTG CTG GAC GCC ACT TTC CGG GGT    209
Val Ser Asp Pro Trp Lys Leu Met Leu Leu Asp Ala Thr Phe Arg Gly
      15                               20                               25

GCA CAG CAA GTG AGT AAC CTG ATC CAC TAC CTG GGA CTG AGC CAT CAC    257
Ala Gln Gln Val Ser Asn Leu Ile His Tyr Leu Gly Leu Ser His His
      30                               35                               40

CTG CTG GCA CTG AAT TTT ATC ATT GTT TCT TTT GGC AAA AAA AGC GCG    305
Leu Leu Ala Leu Asn Phe Ile Ile Val Ser Phe Gly Lys Lys Ser Ala
      45                               50                               55

TGG TCT TCT GCC CAA GTG AAG GTG ACC GAC ACA GAC TTT GAT GGT GTG    353
Trp Ser Ser Ala Gln Val Lys Val Thr Asp Thr Asp Phe Asp Gly Val
      60                               65                               70                               75

GAA GTC AGA GTG TTT GAA GGC CCT CCG AAG CCC GAA GAG CCA CTG AAA    401
Glu Val Arg Val Phe Glu Gly Pro Pro Lys Pro Glu Glu Pro Leu Lys
      80                               85                               90

CGC AGC GTC GTT TAT ATC CAC GGA RGA GGC TGG    434
Arg Ser Val Val Tyr Ile His Gly Xaa Gly Trp
      95                               100

```

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..266

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..257
id H10448
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..266
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..258
id HSC18H071
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..266
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..246
id AA127134
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..266
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..246
id HUML13653
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 47..124
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.3
seq GVGLVTLLGLAVG/SY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

AGGGATCTGT CGGCTTGTC	GGTGGTGGAG	GAAAAGGCGC	TCCGTC	ATG GGG ATC	55
				Met Gly Ile	
				-25	
CAG ACG AGC CCC GTC CTG CTG GCC TCC CTG GGG GTG GGG CTG GTC ACT					103
Gln Thr Ser Pro Val Leu Leu Ala Ser Leu Gly Val Gly Leu Val Thr					
-20	-15			-10	
CTG CTC GGC CTG GCT GTG GGC TCC TAC TTG GTT CGG AGG TCC CGC CGG					151
Leu Leu Gly Leu Ala Val Gly Ser Tyr Leu Val Arg Arg Ser Arg Arg					
-5	1		5		
CCT CAG GTC ACT CTC CTG GAC CCC AAT GAA AAG TAC CTG CTA CGA CTG					199
Pro Gln Val Thr Leu Leu Asp Pro Asn Glu Lys Tyr Leu Leu Arg Leu					
10	15		20	25	
CTA GAC AAG ACG ACT GTG AGC CAC AAC ACC AAG AGG TTC CGC TTT GCC					247
Leu Asp Lys Thr Thr Val Ser His Asn Thr Lys Arg Phe Arg Phe Ala					

CTG CCC ACC GCC CAC CAC ATG
Leu Pro Thr Ala His His Met
45

268

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 53..91
id N86348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..40
id N86348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 227..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 211..241
id N86348
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..154
id N88408
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide

(B) LOCATION: 52..258
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: _score 6.3
 seq ILLIVLFLDAVRE/VR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

AGCGGRSAGC GCAGGGAGCC AGGCGGGCTG CCGCGGGTG TGAAGAAAAA A ATG ACA      57
                                   Met Thr

CTC CAA TGG GCT GCA GTG GCA ACC TTT CTT TAT GCC GAA ATA GGA CTC      105
Leu Gln Trp Ala Ala Val Ala Thr Phe Leu Tyr Ala Glu Ile Gly Leu
      -65                               -60                               -55

ATT TTA ATC TTC TGC CTA CCT TTT ATT CCT CCT CAG AGA TGG CAG AAG      153
Ile Leu Ile Phe Cys Leu Pro Phe Ile Pro Pro Gln Arg Trp Gln Lys
      -50                               -45                               -40

ATT TTT TCA TTT AAT GTC TGG GGT AAA ATT GCA ACT TTT TGG AAC AAG      201
Ile Phe Ser Phe Asn Val Trp Gly Lys Ile Ala Thr Phe Trp Asn Lys
      -35                               -30                               -25                               -20

GCT TTC CTT ACC ATT ATC ATC CTA TTG ATT GTT CTA TTT CTA GAT GCT      249
Ala Phe Leu Thr Ile Ile Ile Leu Leu Ile Val Leu Phe Leu Asp Ala
      -15                               -10                               -5

GTG AGA GAA GTA AGG AAA TAT TCC TCA GTT CAT ACC ATT GAG AAG AGC      297
Val Arg Glu Val Arg Lys Tyr Ser Ser Val His Thr Ile Glu Lys Ser
      1                               5                               10

TCC ACC AGC AGA CCA AGG
Ser Thr Ser Arg Pro Arg
      15
  
```

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..138
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
 region 1..122
 id HSC3DD031
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 137..188
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 120..171
id HSC3DD031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 136..188
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 83..135
id T75196
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 92..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 38..85
id T75196
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 89..343
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq FLDFCVYIPLSWG/FC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```
AAGAAGCCTG TGTGGCCTTC CCGGCGGCTG ATTCGAGGGC TTGTTTGGTC AGAAGGGGGG    60
CGTCAGAGAA GCTGCCCCCTT AGCCAACC ATG CCG TCT GAG GGT CGC TGC TGG    112
                               Met Pro Ser Glu Gly Arg Cys Trp
                               -85                               -80

GAG ACC TTG AAG GCC CTA CGC AGT TCC GAC AAA GGT CGC CTT TGC TAC    160
Glu Thr Leu Lys Ala Leu Arg Ser Ser Asp Lys Gly Arg Leu Cys Tyr
      -75                               -70                               -65

TAC CGC GAC TGG CTG CTG CGG CGC GAG GTG AGC GGT GGC CCC GGA GGA    208
Tyr Arg Asp Trp Leu Leu Arg Arg Glu Val Ser Gly Gly Pro Gly Gly
      -60                               -55                               -50

CGT AGG CCT TTC CGG CCC CTC GCG ACC GAA ACC TTC TCC CTA GCC GTT    256
Arg Arg Pro Phe Arg Pro Leu Ala Thr Glu Thr Phe Ser Leu Ala Val
      -45                               -40                               -35                               -30

GGC ACG TTC TGC TCC CGG GAA CCC GTG CAG TCT AAC AAC CTG CAT TTA    304
Gly Thr Phe Cys Ser Arg Glu Pro Val Gln Ser Asn Asn Leu His Leu
      -25                               -20                               -15

TTT CTT GAC TTC TGT GTG TAC ATC CCT CTG TCC TGG GGT TTC TGT CCT    352
Phe Leu Asp Phe Cys Val Tyr Ile Pro Leu Ser Trp Gly Phe Cys Pro
```

-10

-5

1

CTT CAG CCT ATT TTA GCG
Leu Gln Pro Ile Leu Ala
5

370

(2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 207..292
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 217..302
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 308..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 318..391
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 111..182
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 38..104
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 52..118
id N92143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..41

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 1..30
id N92143
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 119..293
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 91..265
id R97442
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 2..98
id R97442
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 293..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 264..352
id R97442
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(254..378)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..125
id R97398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(146..253)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 125..232
id R97398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(97..147)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 232..282
id R97398
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 119..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 90..276
id T80897
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..97
id T80897
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 26..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..100
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 119..169
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 93..143
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 246..289
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 219..262
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 203..245
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 175..217
id AA047755
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 169..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 142..176
id AA047755
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..116
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq AILGSTWVALTTG/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

AATCCGGGCC GCGCGGGGAA GGGGAGACGT GGGGTAGAGT GACC ATG ACG AAA TTA      56
                                   Met Thr Lys Leu

GCG CAG TGG CTT TGG GGA CTA GCG ATC CTG GGC TCC ACC TGG GTG GCC      104
Ala Gln Trp Leu Trp Gly Leu Ala Ile Leu Gly Ser Thr Trp Val Ala
-20                               -15                -10                -5

CTG ACC ACG GGA GCC TTG GGC CTG GAG CTG CCC TTG TCC TGC CAG GAA      152
Leu Thr Thr Gly Ala Leu Gly Leu Glu Leu Pro Leu Ser Cys Gln Glu
                               1                   5                   10

GTC CTG TGG CCA CTG CCC GCC TAC TTG CTG GTG TCC GCC GGC TGC TAT      200
Val Leu Trp Pro Leu Pro Ala Tyr Leu Leu Val Ser Ala Gly Cys Tyr
                               15                   20                   25

GCC CTG GGC ACT GTG GGC TAT CGT GTG GCC ACT TTT CAT GAC TGC GAG      248
Ala Leu Gly Thr Val Gly Tyr Arg Val Ala Thr Phe His Asp Cys Glu
                               30                   35                   40

GAC GCC GCA CGC GAG CTG CAG AGC CAG ATA CAG GAG GCC CGA GCC GAC      296
Asp Ala Ala Arg Glu Leu Gln Ser Gln Ile Gln Glu Ala Arg Ala Asp
                               45                   50                   55                   60

TTA GCC CGC ANG GGC TGC GCT TCT GAC AGC CTA ASC CCA TTC CTG TGC      344
Leu Ala Arg Xaa Gly Cys Ala Ser Asp Ser Leu Xaa Pro Phe Leu Cys
                               65                   70                   75

GGA CAG CCC TTC CTC CCA TTT CCC ATT AAA GAG CCA GGG      383
Gly Gln Pro Phe Leu Pro Phe Pro Ile Lys Glu Pro Gly
                               80                   85

```

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..205

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 28..189
id AA122029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..44
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..30
id AA122029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..232
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 26..211
id HUML1833
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 113..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..128
id AA158721
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 112..174
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq FLVSNMLLA EAYG/SG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```
AAACAAGGGC AGGTCTGACT GCAAGGCTGG GACTGGGAGG CAGAGCCGCC GCCAAGGGGG      60
CCTCGGTAA ACACTGGTCG TTCAATCACC TGCAAGACGA AGGAGGCAAG G ATG CTG      117
                                     Met Leu
                                     -20

TTG GCC TGG GTA CAA GCA TTC CTC GTC AGC AAC ATG CTC CTA GCA GAA      165
Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu Ala Glu
      -15                               -10                               -5

GCC TAT GGA TCT GGA GGC TGT TTC TGG GAC AAC GGC CAC CTG TAC CGG      213
Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu Tyr Arg
      1                               5                               10

GAG GAC CAG ACC TCC CCC GCG CCG GGC CTC CGC TGC CTC AAC TGG CTG      261
Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn Trp Leu
      15                               20                               25
```

GAC GCA CAG AGC GGG
Asp Ala Gln Ser Gly
30

276

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 63..212
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 206..338
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 393..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 401..452
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 30..60
id R85337
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..366
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 26..345
id T86800
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 373..403
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 354..384
id T86800
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 46..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 49..381
id H94753
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 65..187
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq SVLVLLLLLAVLYE/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

AGACTCGGAG CGAGGAGACC CGAGCGAGCA GACGCGGCCC TGGCGCCCGC CCTGCGCACT	60
CACC ATG GCG ATG CAT TTC ATC TTC TCA GAT ACA GCG GTG CTT CTG TTT	109
Met Ala Met His Phe Ile Phe Ser Asp Thr Ala Val Leu Leu Phe	
-40 -35 -30	
CAT TTC TGG AGT GTC CAC AGT CCT GCT GGC ATG GCC CTT TCG GTG TTG	157
His Phe Trp Ser Val His Ser Pro Ala Gly Met Ala Leu Ser Val Leu	
-25 -20 -15	
GTG CTC CTG CTT CTG GCT GTA CTG TAT GAA GGC ATC AAG GTT GGC AAA	205
Val Leu Leu Leu Leu Ala Val Leu Tyr Glu Gly Ile Lys Val Gly Lys	
-10 -5 1 5	
GCC AAG CTG CTC AAC CAG GTA CTG GTG AAC CTG CCA ACC TCC ATC AGC	253
Ala Lys Leu Leu Asn Gln Val Leu Val Asn Leu Pro Thr Ser Ile Ser	
10 15 20	
CAG CAG ACC ATC GCA GAG ACA GAC GGG GAC TCT GCA GGC TCA GAT TCA	301
Gln Gln Thr Ile Ala Glu Thr Asp Gly Asp Ser Ala Gly Ser Asp Ser	
25 30 35	
TTC CCT GTT GGC AGA ACC CAC CAC AGG TGG TAT TTG TGT CAC TTT GGC	349
Phe Pro Val Gly Arg Thr His His Arg Trp Tyr Leu Cys His Phe Gly	
40 45 50	
CAG TCT CTA ATC CAT GTC ATC CAG GTG GTC ATC GGC TAC TTC ATC ATG	397
Gln Ser Leu Ile His Val Ile Gln Val Val Ile Gly Tyr Phe Ile Met	
55 60 65 70	

CTG GCC GTA ATG TCC TAC AAC ACC TGG ATT TTC CTT GGT GTG GTC
Leu Ala Val Met Ser Tyr Asn Thr Trp Ile Phe Leu Gly Val Val
75 80 85

442

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 183..278
id T97803
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 5..84
id N89398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(300..345)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 273..318
id T97702
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 163..387
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.2
seq VVXXSVLXTTCXS/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGGGGCAGCG CGGGCTGCC ATGGCTGAGC TGCAGCAGCT CCGGGTGCAG GAGGCGGTGG 60
AGTCCATGGT GAAAGTCTG GAAAGAGAGA ACATCCGGAA GATGCAGGGT CTCATGTTCC 120

```

GGTGCAGCGS CAGCYTGTTK GTVAAAGRMC AGCMAGGCCT CC ATG AAG CAG GTG      174
                                   Met Lys Gln Val
                                   -75

CAC CAG TGC ATC GAG CGC TGC CAT GTG CCT CTG GCT CAA GCC CAG GCT      222
His Gln Cys Ile Glu Arg Cys His Val Pro Leu Ala Gln Ala Gln Ala
-70                               -65                               -60

TTG GTC ACC AGT GAG CTG GAG AAG TTC CAG GAC CGC CTG GCC CGG TGC      270
Leu Val Thr Ser Glu Leu Glu Lys Phe Gln Asp Arg Leu Ala Arg Cys
-55                               -50                               -45                               -40

ACC ATG CAT TGC AAC GAC AAA GCC AAA GAT TCA ATA GAT GCT GGG WGT      318
Thr Met His Cys Asn Asp Lys Ala Lys Asp Ser Ile Asp Ala Gly Xaa
-35                               -30                               -25

AAG GAG CTT CAG GTG AAG CAG CAG CTG AMA GTT GTG TKR MCA AGT GTG      366
Lys Glu Leu Gln Val Lys Gln Gln Leu Xaa Val Val Xaa Xaa Ser Val
-20                               -15                               -10

TTG RTG ACC ACA TGC AMC TCA TCC CAA CTA      396
Leu Xaa Thr Thr Cys Xaa Ser Ser Gln Leu
-5                               1

```

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..179
id AA058587
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..193
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..161
id R20025
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 38..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..89
id R12128
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..193
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 87..156
id R12128
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..193
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 2..155
id H19999
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 78..193
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..116
id H83838
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 76..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.2
seq LLAALMLVAMLQL/LY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```
AAAATCCGGG CTTGCGGCCG CTGGCGTAGT CTGTGGCCGG GTGGTCGTTG CTGCGCGCCC      60
CGAGCCCCGA GAGCC ATG CAG ATG TCC TAC GCC ATC CGG TGC GCC TTC TAC      111
           Met Gln Met Ser Tyr Ala Ile Arg Cys Ala Phe Tyr
                   -25                               -20

CAG CTG CTG CTG GCC GCG CTC ATG CTG GTG GCG ATG CTG CAG CTG CTC      159
Gln Leu Leu Leu Ala Ala Leu Met Leu Val Ala Met Leu Gln Leu Leu
-15                   -10                   -5                               1

TAC CTG TCG CTG CTG TCC GGA CTA CAC GGG CCG      192
Tyr Leu Ser Leu Leu Ser Gly Leu His Gly Pro
           5                               10
```

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..324
id AA143123
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(192..316)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 312..436
id AA142922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(310..376)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 253..319
id AA142922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(142..191)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 436..485
id AA142922
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(130..327)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 7..204
id H54590
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 241..376

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 10..145
id AA013161
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 241..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 10..145
id AA018245
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 198..254
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```
AAGTAGCAGA GGCAGCTTCT GAGAGCCTGG GCAGGCAGCA GCTGGCTGAC CAAGTCCACT    60
GGAAGAGAAG GCTTGTGCCA GCCGGGAGAA GGAAGCCGGG GACAGGATGR RAGCAACAAC    120
ACCTTTGCAG ACASTCGACC GGCCCAAGGA CTGGTACAAG ACGATGTTTA AGCAAATTCA    180
CATGGTGCAC AAGCCGG ATG ATG ACA CAG ACA TGT ATA ATA CTC CTT ATA    230
              Met Met Thr Gln Thr Cys Ile Ile Leu Leu Ile
              -15                               -10

CAT ACA ATG CAG GTC TGT ACA ACC CAC CCT ACA GTG CTC AGT CAC ACC    278
His Thr Met Gln Val Cys Thr Thr His Pro Thr Val Leu Ser His Thr
              -5                               1                               5

CTG CTG CAA AGA CCC AAA CCT ACA GAC CTC TTT CCA AAA GCC ACT CCG    326
Leu Leu Gln Arg Pro Lys Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro
              10                               15                               20

ACA ACA GCC CCA ATG CCT TTA AGG ATG CGT CCT CCC CAG TGC CTC CCC    374
Thr Thr Ala Pro Met Pro Leu Arg Met Arg Pro Pro Gln Cys Leu Pro
              25                               30                               35                               40

GAG
Glu                                                    377
```

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 488 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 109..425
id AA037143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..110
id AA037143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 443..483
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 423..463
id AA037143
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 121..287
id W37233
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..482
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 367..479
id W37233
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 293..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 287..324
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..57
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 15..50
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..128
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 89..122
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 67..96
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 60..89
id W37233
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 128..424
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 100..396
id N78012
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..128
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 34..101
id N78012
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 417..464
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 390..437
id N78012
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 29..60
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..32
id N78012
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..330
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 107..309
id W52332
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 353..482
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 335..464
id W52332
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..108
id W52332
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 116..305
id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..128
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 28..96
id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 128..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 95..135
id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 432..467
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 406..441

id AA081257
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 372..437
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq LFLTCLFWPLAAL/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

```
AGACACTTCC TGGTGGGATC CGAGTGAGGC GACGGGGTAG GGGTTGGCGC TCAGGCGGCG 60
ACCATGGCGT ATCACGGCCT CACTGTGCCT CTCATTGTGA TGAGCGTGTT CTGGGGCTTC 120
GTCGGCTTTC TTGGTGCCTT GGTTCATCCC TAAGGGTCCT AACCGGGGAG TTATCATTAC 180
CATGTTGGTG ACCTGTTTAC TTTGCTGCTA TCTCTTTTGG CTGATTGCAA TTCTGGCCCA 240
ACTCAACCCT CTCTTTGGAC CGCAATTGAA AAATGAAACC ATCTGGTATC TGAAGTATCA 300
TTGGCCTTGA GGAAGAAGAC ATGCTCTACA GTGCTCAGTC TTTGAGGTCA CGAGAAGAGA 360
ATGCCTTCTA G ATG CRN DAT CAC CTC CAA ACC AGA CCA CTT TTC TTG ACT 410
      Met Xaa Xaa His Leu Gln Thr Arg Pro Leu Phe Leu Thr
            -20                      -15                      -10

TGC CTG TTT TGG CCA TTA GCT GCC TTA AAC GTT AAC AGC ACA TTT GAA 458
Cys Leu Phe Trp Pro Leu Ala Ala Leu Asn Val Asn Ser Thr Phe Glu
            -5                      1                      5

TGC CTT ATT CTA CAA TGC AGC GTG GGG ATC 488
Cys Leu Ile Leu Gln Cys Ser Val Gly Ile
      10                      15
```

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..265
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 139..237
id T53688
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 103..175
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 74..146
id T53688
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 179..334
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq LMAFLLSFYLIPT/NE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

```
AATGCGCAGA AACACTGGGC ACAGGGGGAG GTAAGTGCAG TAAGTCCCGC TTGGCCCTGG      60
AGTCCACGCG GATTTTCGAA GCTGGGGCTG GCAAGAGGCC GCTGGACACC ACGCTCCAGT     120
CGTCAGCCCA CTTCTAGCT GAACAGCGCG AGGCGGCGGC AGCGAGCCGG GTCCCACC      178
ATG GCC GCG AAT TAT TCC AGT ACC ART ACC CGG AGA GAA CAT GTC AAA      226
Met Ala Ala Asn Tyr Ser Ser Thr Xaa Thr Arg Arg Glu His Val Lys
   -50                      -45                      -40

GTT AAA ACC AGC TCC CAG CCA GGC TTC CTG GAA CGG CTG AGC GAG ACC      274
Val Lys Thr Ser Ser Gln Pro Gly Phe Leu Glu Arg Leu Ser Glu Thr
   -35                      -30                      -25

TCG GGT GGG ATG TTT GTG GGG CTC ATG GCC TTC CTG CTC TCC TTC TAC      322
Ser Gly Gly Met Phe Val Gly Leu Met Ala Phe Leu Leu Ser Phe Tyr
   -20                      -15                      -10                      -5

CTA ATT TTC ACC AAT GAG GGC CGC GCA TTG AAG ACG GCA ACC TCA TTG      370
Leu Ile Phe Thr Asn Glu Gly Arg Ala Leu Lys Thr Ala Thr Ser Leu
               1               5               10

GCT GAG GGG CTC TCG CTT GTN GTG TCT CCC GAC AGC ATC CAC AGT GTG      418
Ala Glu Gly Leu Ser Leu Val Val Ser Pro Asp Ser Ile His Ser Val
   15               20               25

GCT CCG GAG AAT GAA GGA ANG CTG GTG CAC ATC ATT      454
Ala Pro Glu Asn Glu Gly Xaa Leu Val His Ile Ile
   30               35               40
```

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 15..215
id W04921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 247..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 227..309
id W04921
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(60..284)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 216..440
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(287..329)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 172..214
id N70602
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 83..221
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..139
id W70167
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 264..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 183..248
id W70167
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 84..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..131
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 247..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 165..247
id W37690
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 253..315
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.1
seq LEMLTAFASHIRA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

```
AACGAGTTCT TCCGGGGCGG AGGTCACCAT GGCAGCTGCC TTGGCTCGGC TTGGTCTGCG      60
GCCTGTCAAA CAGGTTCTGGG TTCAGTTCTG TCCCTTCGAG AAAAACGTGG AATCGACGAG     120
GACCTTCCTG CAGACGGTGA GCAGTGAGAA GGTCCGCTCC ACTAATCTCA ACTGCTCAGT     180
GATTGCGGAC GTGAGGCATG ACGGCTCCGA GCCCTGCGTG GACGTGCTGT TCGGAACGGG     240
CATCGCCTGA TT ATG CGC GGC GCT CAT CTC ACC GCT CTG GAA ATG CTC ACC     291
      Met Arg Gly Ala His Leu Thr Ala Leu Glu Met Leu Thr
      -20                      -15                      -10

GCC TTC GCC TCC CAC ATC CGG GCC AGG GAC GCA TCG GGG                      330
Ala Phe Ala Ser His Ile Arg Ala Arg Asp Ala Ser Gly
      -5                      1                      5
```

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 228..367

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 143..282
id AA143123
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 89..206
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..118
id AA143123
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(228..360)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 7..139
id H54590
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(166..206)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 164..204
id H54590
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(201..349)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 312..460
id AA142922
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..367
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 10..103
id AA013161
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..367
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 10..103
id AA018245
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 216..287
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.1
seq IILLIHTMQVCTT/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

```

AAGTGTATCT GGGCAGCCCC TTCCGGCAAA ACGCAGCAGT AGCAGAGGCA GCTTCTGAGA    60
GCCTGGGCAG GCAGCAGCTG GCTGACCAAG TCCACTGGAA GAGAAGGCTT GTGCCAGCCG    120
GGAGAAGGAA GCCGGGGACA GGATGAAAGC AACAACACCT TTGCAGACAG TCGACCGGCC    180
CAAGGACTGG TACAAGACGA TGTTAAGCAA TTCAC ATG GTG CAC AAG CCG ATG        233
                               Met Val His Lys Pro Met
                               -20

ATG ACA CAG ACA TGT ATA ATA CTC CTT ATA CAT ACA ATG CAG GTC TGT      281
Met Thr Gln Thr Cys Ile Ile Leu Leu Ile His Thr Met Gln Val Cys
-15                               -10                               -5

ACA ACC CAC CCT ACA GTG CTC AGT CAC ACC CTG CTG CAA AGA CCC AAA      329
Thr Thr His Pro Thr Val Leu Ser His Thr Leu Leu Gln Arg Pro Lys
1                               5                               10

CCT ACA GAC CTC TTT CCA AAA GCC ACT CCG ACA ACA                      365
Pro Thr Asp Leu Phe Pro Lys Ala Thr Pro Thr Thr
15                               20                               25

```

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 85..197
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 85..197
id N43024
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 17..84
id N43024
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 97..189
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 80..172
id T62095
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 51..96
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 35..80
id T62095
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 16..50
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..35
id T62095
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 51..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 26..172
id W42796
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 114..211
id AA030227
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..197
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 51..148
id AA118270
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..177

(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq IGLMFLMLGCALP/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```

GTTGTCTGGC CGCCGTAGCG CGTCTTGGGT CTCCCGGCTG CCGCTGCTGC CGCCGCCGCC      60
TCGGGTCGTG GAGCCAGGAG CGACGTCACC GCC ATG GCA GGC ATC AAA GCT TTG      114
                               Met Ala Gly Ile Lys Ala Leu
                               -25

ATT AGT TTG TCC TTT GGA GGA GCA ATC GGA CTG ATG TTT TTG ATG CTT      162
Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu Met Phe Leu Met Leu
-20                      -15                      -10

GGA TGT GCC CTT CCA ATA TAC AAC AAA TAC TGG CCT ACG      201
Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp Pro Thr
-5                      1                      5
```

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 135..268
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 119..252
id W20516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..92
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 12..79
id W20516
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 352..391
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 343..382

id W20516
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..433
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 393..425
id W20516
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..122
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 79..108
id W20516
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 203..471
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 420..688
id HSZ78368
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..106
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 46..124
id HSZ78368
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 151..220
id HSZ78368
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 135..303
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 132..300
id R82255
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..106
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91
region 24..105
id R82255
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..31
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 2..31
id R82255
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 205..471
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 55..321
id H99530
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 203..358
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 391..546
id AA209097
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 208..270
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6
seq LLFPLTLVRSFWS/DM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```
AAGAGGGGAA CAAGATGGCG GCGCCGAAGG GGAGCCTCTG GGTGAGGACC CAACTGGGGC 60
TCCCGCCGCT GCTGCTGCTG ACCATGGCCT TGGCCGGAGG TTCGGGGACC GCTTCGGCTG 120
AAGCATTTGA CTCGGKCYTG GKKRATACG GCGTCTTGCC ACCGGGCCTG TCAGTTGACC 180
TACCCCTTGC ACACCTACCC TAAGCTT ATG TCC CTG ATG CCA AAA ATG CAC CTA 234
                Met Ser Leu Met Pro Lys Met His Leu
                -20                      -15

CTC TTT CCT CTA ACT CTG GTG AGG TCA TTC TGG AGT GAC ATG ATG GAC 282
Leu Phe Pro Leu Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp
    -10                      -5                      1

TCC GCA CAG AGC TTC ATA ACC TCT TCA TGG ACT TTT TAT CTT CAA GCC 330
Ser Ala Gln Ser Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala
    5                      10                      15                      20

GAT GAC GGR AAA ATA GTT ATA TTC CAG TCT AAG CCA GAA ATC CAG TAC 378
```

Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	
				25					30					35		
GCA	CCA	CAT	TTG	GAG	CAG	GAG	CCT	ACA	AAT	TTG	AGA	GAA	TCA	TCT	CTA	426
Ala	Pro	His	Leu	Glu	Gln	Glu	Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	
			40				45						50			
AGC	AAA	ATG	TCC	TAT	CTG	CAA	ATG	AGA	AAT	TCA	CAA	GCG	CAC	AGG		471
Ser	Lys	Met	Ser	Tyr	Leu	Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg		
		55					60					65				

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 382 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 123..407
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 69..119
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 38..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.9
seq SNILLASVGSVLG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

ATTTCCTGGG	CCAAGTTGGG	ACCCGGACGG	CCTCACC	ATG	ATG	AAA	CGG	GCA	GCT	
				Met	Met	Lys	Arg	Ala	Ala	55
										-85

GCT	GCT	GCA	GTG	GGA	GGA	GCC	CTG	GCA	GTG	GGG	GCT	GTG	CCC	GTG	GTG	103
Ala	Ala	Ala	Val	Gly	Gly	Ala	Leu	Ala	Val	Gly	Ala	Val	Pro	Val	Val	

-80

-75

-70

CTC	AGT	GCC	ATG	GGC	TTC	ACT	GGG	GCA	GGA	ATC	GCC	GCG	TCC	TCC	ATA	151
Leu	Ser	Ala	Met	Gly	Phe	Thr	Gly	Ala	Gly	Ile	Ala	Ala	Ser	Ser	Ile	
-65					-60					-55					-50	
GCA	GCC	AAG	ATG	ATG	TCC	GCA	GCA	GCC	ATT	GCC	AAC	GGG	GGT	GGT	GTT	199
Ala	Ala	Lys	Met	Met	Ser	Ala	Ala	Ala	Ile	Ala	Asn	Gly	Gly	Gly	Val	
			-45						-40					-35		
TCT	GCG	GGG	AGC	CTG	GTG	GCT	ACT	CTG	CAG	TCC	GTG	GGG	GCA	GCT	GGA	247
Ser	Ala	Gly	Ser	Leu	Val	Ala	Thr	Leu	Gln	Ser	Val	Gly	Ala	Ala	Gly	
			-30					-25					-20			
CTC	TCC	ACA	TCA	TCC	AAC	ATC	CTC	CTG	GCC	TCT	GTT	GGG	TCA	GTG	TTG	295
Leu	Ser	Thr	Ser	Ser	Asn	Ile	Leu	Leu	Ala	Ser	Val	Gly	Ser	Val	Leu	
		-15					-10					-5				
GGG	GCC	TGC	TTG	GGG	AAT	TCA	CCT	TCH	KCT	TCT	CTC	CCA	GCT	GAA	CCC	343
Gly	Ala	Cys	Leu	Gly	Asn	Ser	Pro	Ser	Xaa	Ser	Leu	Pro	Ala	Glu	Pro	
	1				5				10						15	
GAB	GKN	DAA	GAA	GAT	GAG	GCA	AGA	GAA	AAT	GTA	CCG	CCG				382
Xaa	Xaa	Xaa	Glu	Asp	Glu	Ala	Arg	Glu	Asn	Val	Pro	Pro				
			20					25								

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 117..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 102..301
id H10706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 6..101
id H10706
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 74..273
id AA043571
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 42..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..73
id AA043571
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 99..298
id W63643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 18..98
id W63643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..316
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 38..237
id AA081648
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..265
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 83..236
id HUMHBC2885
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..87
id HUMHBC2885
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 220..261
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.8
seq VTIILLSCXFWA/VK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
AAAGTAGGGC TGGCGTASGG CCGCCATGTT GCAGCAGGAT AGTAATGATG AACTGAAGA    60
TGTTTCACTG TTTGATGCGG AAGAGGAGAC GACTAATAGA CCAAGRWAAG CCRAVDRRTC  120
AGRCGTCCAG TAGCRTCGTT TTTCCACTTA TTCTTTCGAG TCAGTGCAAT SATCGTCTAT  180
CTTCTCTGTG AGTTGSTCAG CAGCAGCTTT ATTACCTGT ATG GTG ACA ATT ATC      234
                                   Met Val Thr Ile Ile
                                   -10

TTG TTG TTG TCG TGT GRC TTT TGG GCA GTG AAG AAT GTC ACA KGT AGA      282
Leu Leu Leu Ser Cys Xaa Phe Trp Ala Val Lys Asn Val Thr Xaa Arg
               -5                      1                      5

SKA ATG GTT GGC CTA CGT TGG TGG AAT CAC ATT                          315
Xaa Met Val Gly Leu Arg Trp Trp Asn His Ile
              10                      15
```

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 76..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 123..447
id W52706
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..71
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 69..119
id W52706

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 14..274
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.8
 seq SNILLASVGSVSG/AC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```

AGACGGCCTC ACC ATG AWR AAA CGG GCA GCT GCT GCT GCA GTG GGA GGA      49
      Met Xaa Lys Arg Ala Ala Ala Ala Ala Val Gly Gly
              -85                      -80

GCC CTG GCA GTG GGG GCT GTG CCC GTG GTG CTC AGT GCC ATG GGC TTC      97
Ala Leu Ala Val Gly Ala Val Pro Val Val Leu Ser Ala Met Gly Phe
-75              -70                      -65                      -60

ACT GGG GCA GGA ATC GCC GCG TCC TCC ATA GCA GCC AAG ATG ATG TCC      145
Thr Gly Ala Gly Ile Ala Ala Ser Ser Ile Ala Ala Lys Met Met Ser
              -55                      -50                      -45

GCA GCA GCC ATT GCC AAC GGG GGT GGT GTT TCT GCG GGG AGC CTG GTG      193
Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ser Ala Gly Ser Leu Val
              -40              -35                      -30

GCT ACT CTG CAG TCC GTG GGG GCA GCT GGA CTC TCC ACA TCA TCC AAC      241
Ala Thr Leu Gln Ser Val Gly Ala Ala Gly Leu Ser Thr Ser Ser Asn
              -25              -20                      -15

ATC CTC CTG GCC TCT GTT GGG TCA GTG TCG GGG GCC TGC TTG GGG AAT      289
Ile Leu Leu Ala Ser Val Gly Ser Val Ser Gly Ala Cys Leu Gly Asn
              -10              -5              1              5

TCA CCT TCT TCT TCT CTC CCA GCT GAA CCC GAG GCT AAA GAA GAT GAG      337
Ser Pro Ser Ser Ser Leu Pro Ala Glu Pro Glu Ala Lys Glu Asp Glu
              10              15              20

GCA AGA GAA AAT GTA CCC CAA GGT GAA CCT CCA AAA CCC CCA CTC AAG      385
Ala Arg Glu Asn Val Pro Gln Gly Glu Pro Pro Lys Pro Pro Leu Lys
              25              30              35

TCA GAG AAA CAT GAG CGG      403
Ser Glu Lys His Glu Arg
              40

```

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 239..342
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 134..237
id AA218802
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 129..218
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 22..111
id AA218802
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 86..352
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq DLSLLSLPPGTSP/VG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
AGGCGGCATT TCGGCCCGGC GCCAGGGTGG AGAGTTGTGC GCCGGTCCCT GGGCCTGAGC      60
TCCGGCTCCG GCTGGGGCGC CTGCG ATG TCT CAA GAT GGC GGA STG GGC GAA      112
                Met Ser Gln Asp Gly Gly Xaa Gly Glu
                -85
TTA AAG CAC ATG GTG ATG AGT TTC CGG GTG TCT GAG CTC CAG GTG CTT      160
Leu Lys His Met Val Met Ser Phe Arg Val Ser Glu Leu Gln Val Leu
-80                -75                -70                -65
CTT GGC TTN SCT GGC CGG AAC AAG AGT GGA CGG AAG CAC GAG CTC CTG      208
Leu Gly Xaa Xaa Gly Arg Asn Lys Ser Gly Arg Lys His Glu Leu Leu
                -60                -55                -50
GCC AAG GCT CTG CAC CTC CTG AAG TCC AGC TGT GCC CCT AGT GTC CAG      256
Ala Lys Ala Leu His Leu Leu Lys Ser Ser Cys Ala Pro Ser Val Gln
                -45                -40                -35
ATG AAG ATC AAA GAG CTT TAC CGA CGA CGC TTT CCC CGG AAG ACC CTG      304
Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg Phe Pro Arg Lys Thr Leu
                -30                -25                -20
GGG CCC TCT GAT CTC TCC CTT CTC TCT TTG CCC CCT GGC ACC TCT CCT      352
Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro
                -15                -10                -5
GTA GGC TCC CCT GGT CCT CTA GCT CCC ATT CCC CCA ACG STG TTG GCK      400
Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Xaa Leu Ala
    1                5                10                15
```

STG GCA MCC TGC TGG GCC CCA AGC GTG AGG TGG ACA TGC
Xaa Ala Xaa Cys Trp Ala Pro Ser Val Arg Trp Thr Cys
20 25.

439

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..301
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 127..268
id W31492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..132
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..101
id W31492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 331..376
id W31492
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..151
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..134
id H85714
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91

region 237..297
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 293..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 187..237
id H85714
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 234..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 119..228
id H52756
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 20..126
id H52756
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..405
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 228..291
id H52756
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 35..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..118
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 234..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 111..220
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..385

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 220..263
id R78970
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..151
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..119
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 288..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 167..222
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 222..265
id R64509
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 268..339
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.7
seq LLLPRVLLTMASG/SL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
AAATCACGTG GCTGCCACCC AGGTAAGAAG AGGCCGCTCT TCCTGGGGTT GTTCTCCGT   60
GTGACGTGTG GCCTTTGAGA TCAACTCTCC TGTACCAGCG TAGGCCGCAT GAGTGGGGGG   120
CGGGCTCCCG CGGTCCTGCT CGGCGGAGTG GTGAGTGACC GGCCCCGCCC CGCCCCTTCC   180
GGTCCTCGAA GCCTCGACCG CTACCCGCAC CCTAAATCCC AGAGGTTGGC CCCCTGAGGT   240
GCCTCTCTGC TCCTGTCTTT TGTTTGG ATG CCG GMG CTG CTG CCT GTG GCC TCM   294
                Met Pro Xaa Leu Leu Pro Val Ala Ser
                -20

CGC CTT TTG TTG CTA CCC CGA GTC TTG CTG ACC ATG GCC TCT GGA AGC   342
Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
-15                -10                -5                1

CTC CGA CYC AGC VCT CGM CGG CCT CGG ATT CCG GMT CTG GCT ACG TTC   390
Leu Arg Xaa Ser Xaa Arg Arg Pro Arg Ile Pro Xaa Leu Ala Thr Phe
```

CGG GMT CGG TCT CTG
Arg Xaa Arg Ser Leu
20

405

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..397
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 54..373
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..98
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..73
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 4..251
id HSC3GD011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 270..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 29..166
id HSC01E081
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 243..274
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: . identity 96
 region 1..32
 id HSC01E081
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 337..407
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..71
 id T05865
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 42..146
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.7
 seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```

GTGTGACTTC GGGCTGTGGG CTCGCTCGCG GCTCTTCGGC C ATG GTT TTC TCA AAC    56
                                   Met Val Phe Ser Asn
                                   -35

AAT GAT GAA GGC CTT ATT AAC AAA AAG TTA CCC AAA GAA CTT CTG TTA    104
Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu Leu Leu Leu
-30                               -25                -20                -15

AGA ATA TTT TCC TTC TTG GAT ATA GTA ACT TTG TGC CGA TGT GCA CAG    152
Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg Cys Ala Gln
                               -10                -5                        1

ATT TYM AAG GCT TGG AAC ATC TTA GCC CTG GAT GGA AGC AAC TGG CAA    200
Ile Xaa Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser Asn Trp Gln
      5                               10                        15

AGA ATA GAT CTT TTT AAC TTT CAA ACA GAT GTA GAG GGT CGA GTG GTG    248
Arg Ile Asp Leu Phe Asn Phe Gln Thr Asp Val Glu Gly Arg Val Val
      20                               25                        30

GAA AAT ATC TCG AAG CGA TGC GGT GGA TTC CTG AGG AAG CTC AGC TTG    296
Glu Asn Ile Ser Lys Arg Cys Gly Gly Phe Leu Arg Lys Leu Ser Leu
      35                               40                        45                        50

CGA GGC TGC ATT GGT GTT GGG GRT TCC TCC TTG RAG ACC TTT GCA CAG    344
Arg Gly Cys Ile Gly Val Gly Xaa Ser Ser Leu Xaa Thr Phe Ala Gln
                               55                60                65

AAC TGC CGA AAC ATT GAA CAT TTG AAC CTC AAT GGA TGC ACA AAA ATC    392
Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys Thr Lys Ile
                               70                75                80

ACT GRC AGC ACG TGT
Thr Xaa Ser Thr Cys
      85

```

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..202
id HSC3GD011
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..224
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 54..175
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..123
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 10..73
id T75227
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 67..171
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq IFSFLDIVTLCRC/AQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```
AAGGACAACG GCGGTCGCMR GCGCCGTGTG ACTTCGGGCT GTGGGCTCGC TCGCGGCTCT    60
TCGGCC ATG GTT TTC TCA AAC AAT GAT GAA GGC CTT ATT AAC AAA AAG    108
      Met Val Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys
      -35                      -30                      -25
TTA CCC AAA GAA CTT CTG TTA AGA ATA TTT TCC TTC TTG GAT ATA GTA    156
```

Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val
-20 -15 -10

ACT TTG TGC CGA TGT GCA CAG ATT TCC AAG GCT TGG AAC ATC TTA GCC 204
Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala
-5 1 5 10

CTG GAT GGA AGC AAC TGG CAG GGG 228
Leu Asp Gly Ser Asn Trp Gln Gly
15

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..312
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 36..323
id W44483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 305..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 317..410
id W44483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 398..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 411..460
id W44483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(181..321)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 233..373
id AA035386

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(323..447)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 108..232
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(109..184)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 371..446
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(10..64)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 494..548
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(77..112)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 444..479
id AA035386
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..420
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 12..417
id H69070
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 416..446
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 414..444
id H69070
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 1..257
id AA057029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..447
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 292..434
id AA057029
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 180..447
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 167..434
id W32750
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..185
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..171
id W32750
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 18..353
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq SSCILPWLSKTNS/CP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

AAGAAGGCTG GGCAGCC ATG GCG TCC TAT TTC GAT GAA CAC GAC TGC GAG	50
Met Ala Ser Tyr Phe Asp Glu His Asp Cys Glu	
-110 -105	
CCG TCG GAC CCT GAG CAG GAG ACG CGA ACC AAC ATG CTG CTG GAG CTC	98
Pro Ser Asp Pro Glu Gln Glu Thr Arg Thr Asn Met Leu Leu Glu Leu	
-100 -95 -90	
GCA AGG TCA CTT TTC AAT AGG ATG GAC TTT GAA GAC TTG GGG TTG GTA	146
Ala Arg Ser Leu Phe Asn Arg Met Asp Phe Glu Asp Leu Gly Leu Val	
-85 -80 -75 -70	
GTA GAT TGG GAC CAC CAC CTG CCT CCA CCA GCT GCC AAG ACT GTG GTT	194
Val Asp Trp Asp His His Leu Pro Pro Pro Ala Ala Lys Thr Val Val	
-65 -60 -55	
GAG AAC CTC CCC AGG ACA GTC ATC AGA GGC TCT CAG GCT GAG CTC AAG	242
Glu Asn Leu Pro Arg Thr Val Ile Arg Gly Ser Gln Ala Glu Leu Lys	
-50 -45 -40	

TGC	CCC	GTG	TGT	CTT	TTG	GAA	TTT	GAG	GAG	GAG	GAG	ACT	GCC	ATT	GAG	290
Cys	Pro	Val	Cys	Leu	Leu	Glu	Phe	Glu	Glu	Glu	Glu	Thr	Ala	Ile	Glu	
		-35					-30					-25				
ATG	CCT	TGC	CAT	CAC	CTT	TTC	CAT	TCC	AGC	TGC	ATT	CTG	CCC	TGG	CTA	338
Met	Pro	Cys	His	His	Leu	Phe	His	Ser	Ser	Cys	Ile	Leu	Pro	Trp	Leu	
		-20				-15					-10					
AGC	AAG	ACA	AAT	TCC	TGT	CCC	TTG	TGC	CGC	TAT	GAG	CTG	CCC	ACT	GAT	386
Ser	Lys	Thr	Asn	Ser	Cys	Pro	Leu	Cys	Arg	Tyr	Glu	Leu	Pro	Thr	Asp	
		-5			1				5					10		
GAC	GAC	ACT	TAT	GAG	GAG	CAC	AGA	CGA	GAT	AAG	GCT	CGA	AAA	CAG	CAG	434
Asp	Asp	Thr	Tyr	Glu	Glu	His	Arg	Arg	Asp	Lys	Ala	Arg	Lys	Gln	Gln	
			15					20					25			
CAG	CAA	CAC	CGA	CCA	NGG											452
Gln	Gln	His	Arg	Pro	Xaa											
					30											

(2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..422
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 12..404
id W22200
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..364
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..332
id R87595
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 129..342
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 96..309
id AA031849

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..123
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 110..286
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..123
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..112
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 49..303
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 74..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 2..53
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 253..297
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

AAAAAGGGG AGGAAATTGA AACTGAGTGG CCCACGATGG GAAGAGGGGA AAGCCCAGGG 60
GTACAGGAGG CCTCTGGGTG AAGGCAGAGG CTAACATGGG GTTCGGAGCG ACCTTGCCCG 120

```

TTGGCCTGAC CATCTTTGTG CTGTCTGTCG TCACTATCAT CATCTGCTTC ACCTGCTCCT 180
GCTGCTGCCT TTACAAGACG TGCCGCCGAC CACGTCCGGT TGTCACCACC ACCACATCCA 240
CCACTGTGGT GC ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT 291
      Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala
      -15                      -10                      -5

ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG 339
Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln
      1                      5                      10

GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT ACC CAC CAC CTT ACC CAG 387
Gly Cys Gln Gln His Pro Thr Gln Cys Ser Thr His His Leu Thr Gln
      15                      20                      25                      30

CCC AGC CCA TGG GCC CAC CGG SCT ACC ACG AGA CCC TGG CTG GAG GAG 435
Pro Ser Pro Trp Ala His Arg Xaa Thr Thr Arg Pro Trp Leu Glu Glu
      35                      40                      45

CAG CCG CGC CCC GGG 450
Gln Pro Arg Pro Gly
      50

```

(2) INFORMATION FOR SEQ ID NO: 194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 85..139
id AA157672
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 219..273
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 86..140
id AA157671
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..94

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 10..47
id HUML116
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 45..263
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LRRLLGCLTLTL/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

AATTGCGTAG TTCCGAATAC CCTCGGCCAC ACCTGGCCTT CTCC ATG CTC GGA ATA	56
Met Leu Gly Ile	
-70	
ACT TCC TGC AGC GAC CAA CAG GCT AAA GAG GGG GAA GGT CTG GAG GGA	104
Thr Ser Cys Ser Asp Gln Gln Ala Lys Glu Gly Glu Gly Leu Glu Gly	
-65 -60 -55	
TCC AGC ACC GGC TCC TCC TCC GGC AAC CAC GGT GGG AGC GGC GGA GGA	152
Ser Ser Thr Gly Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly	
-50 -45 -40	
AAT GGA CAT AAA CCC GGG TGT GAA AAG CCA GGG AAT GAA GCC CGC GGG	200
Asn Gly His Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly	
-35 -30 -25	
AGC GGG AAT CTG GGA TTC AGA ACT CTG AGA CGT CTC CTG GGA TGT TTA	248
Ser Gly Asn Leu Gly Phe Arg Thr Leu Arg Arg Leu Leu Gly Cys Leu	
-20 -15 -10	
ACT TTG ACA CTT TCT GGA AGA ATT	272
Thr Leu Thr Leu Ser Gly Arg Ile	
-5 1	

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91

region 190..271
id AA103102
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..108
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 143..191
id AA103102
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 72..122
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq ALKLASWTSMALA/AS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```
AAATCCCCG CTACCGGGTT GCGCCCGGAA GCCGGGCGCC GCGGCTCTGC TTCCCTCGGG      60
GATCTGGCGA C ATG GCC AGA AAG GCT CTC AAG CTT GCT TCG TGG ACC AGC      110
      Met Ala Arg Lys Ala Leu Lys Leu Ala Ser Trp Thr Ser
      -15                               -10                               -5
ATG GCT CTT GCT GCC TCT GGC ATC TAC TTC TAC AGT AAC AAG TAC TTG      158
Met Ala Leu Ala Ala Ser Gly Ile Tyr Phe Tyr Ser Asn Lys Tyr Leu
      1                               5                               10
GAC CCT AAT GAC TTT GGC GCT GTC AGG GTG GGC AGA GCA GTT GCT ACG      206
Asp Pro Asn Asp Phe Gly Ala Val Arg Val Gly Arg Ala Val Ala Thr
      15                               20                               25
ACG GCT GTC ATC AGT KAC GAC TAC CTC ACT TCC CTG AAG AGT GTC CCT      254
Thr Ala Val Ile Ser Xaa Asp Tyr Leu Thr Ser Leu Lys Ser Val Pro
      30                               35                               40
TAT GGC TCA GAG GAG TAC TTG CAG CTG AGA TCT AAG GTG CAC CTT CGC      302
Tyr Gly Ser Glu Glu Tyr Leu Gln Leu Arg Ser Lys Val His Leu Arg
      45                               50                               55                               60
TCT GCC AGG CGT CTC TGT NAR STC TGC TGT GCC AAC CGG GGC      344
Ser Ala Arg Arg Leu Cys Xaa Xaa Cys Cys Ala Asn Arg Gly
      65                               70
```

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..394
id AA284513
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..332
id H99096
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 363..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 355..395
id H99096
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 13..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..359
id AA020823
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 17..396
id N21197
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 11..277
id AA083141
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 10..57

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6

-seq AALPAWLSLQSR/RS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

CTCGCAGCC ATG GCG GCC GCC GCG CTC CCA GCA TGG CTG TCT CTG CAG TCG      51
Met Ala Ala Ala Ala Leu Pro Ala Trp Leu Ser Leu Gln Ser
      -15                      -10                      -5

AGG GCA AGG TCT CTG CGT GCA TTC TCC ACT GCC GTC TAC TCG GCC ACT      99
Arg Ala Arg Ser Leu Arg Ala Phe Ser Thr Ala Val Tyr Ser Ala Thr
      1                      5                      10

CCG GTC CCG ACA CCT AGC CTG CCG GAA AGA ACA CCC GGA AAT GAA AGG      147
Pro Val Pro Thr Pro Ser Leu Pro Glu Arg Thr Pro Gly Asn Glu Arg
      15                      20                      25                      30

CCA CCA AGN AGA AAG GCA CTA CCT CCT AGG ACA GAG AAA ATG GCT GTT      195
Pro Pro Xaa Arg Lys Ala Leu Pro Pro Arg Thr Glu Lys Met Ala Val
      35                      40                      45

GAC CAG GAC TGG CCT AGT GTT TAC CCA GTT GCA GCA CCA TTB AAA CCC      243
Asp Gln Asp Trp Pro Ser Val Tyr Pro Val Ala Ala Pro Xaa Lys Pro
      50                      55                      60

TCT GCA GTA CCT CTT CCT GTT CGA ATG GGT TAT CCA GTA AAA AAG GGC      291
Ser Ala Val Pro Leu Pro Val Arg Met Gly Tyr Pro Val Lys Lys Gly
      65                      70                      75

GTG CCC ATG GCA AAG GAG GGA AAT CTA GAA CTT TTA AAG ATT CCC AAT      339
Val Pro Met Ala Lys Glu Gly Asn Leu Glu Leu Leu Lys Ile Pro Asn
      80                      85                      90

TTT CTG CAT TTG ACT CCT GTA GCA ATT AAA AAG CAC TGT GNR GCC CTT      387
Phe Leu His Leu Thr Pro Val Ala Ile Lys Lys His Cys Xaa Ala Leu
      95                      100                      105                      110

AAA GAT TTT TGC ACT GAG      405
Lys Asp Phe Cys Thr Glu
      115

```

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 453 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 92..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: . identity 97
region 83..446
id W37917
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 5..85
id W37917
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..446
id AA010474
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..84
id AA010474
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 79..289
id W77834
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 368..455
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 345..432
id W77834
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 32..106
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 6..80
id W77834
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..373
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 288..349
id W77834
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 103..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 85..374
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 3..74
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 389..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 370..436
id N78175
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 183..455
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 158..430
id AA169869
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 30..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..66
id AA169869
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 140..190
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 114..164
id AA169869

est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 104..144
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 77..117
 id AA169869
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 118..312
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq CMLTLXXLSFILA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

GTAGTGTTAG ACTGAAGATA AAGTAAGTGC TGTTTGGGCT AACAGGATCT CCTCTTGCAG      60
TCTGCAGCCC AGGACGCTGA TTCCAGCAGC GCCTTACCGC GCASCCGAAG ATTCACT      117
ATG GTG AAA ATC GCC TTC AAT ACC CCT ACC GCC GTG CAA AAG GAG GAG      165
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu Glu
-65                      -60                      -55                      -50
GCG CGG CAA GAC GTG GAG GCC CTC CTG AGC CGC ACG GTC AGA ACT CAG      213
Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg Thr Gln
-45                      -40                      -35
ATA CTG ACC GGC AAG GAG CTC CGA GTT GCC ACC CAG GAA AAA GAG GGC      261
Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu Lys Glu Gly
-30                      -25                      -20
TCC TCT GGG AGA TGT ATG CTT ACT CTC TTN NVC CTT TCA TTC ATC TTG      309
Ser Ser Gly Arg Cys Met Leu Thr Leu Xaa Xaa Leu Ser Phe Ile Leu
-15                      -10                      -5
GCA GGA CTT ATT GTT GGT GGA GCC TGC ATT TAC AAG TAC TTC ATG CCC      357
Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr Lys Tyr Phe Met Pro
1                      5                      10                      15
AAG AGC ACC ATT TAC CGT GGA NAG ATG TGC TTT TTT GAT TCT GAG GAT      405
Lys Ser Thr Ile Tyr Arg Gly Xaa Met Cys Phe Phe Asp Ser Glu Asp
20                      25                      30
CCT GCA AAT TCC CTT CGT GGA GGA GAG CCT AAC TTC CTG CCT GTG ACT      453
Pro Ala Asn Ser Leu Arg Gly Gly Glu Pro Asn Phe Leu Pro Val Thr
35                      40                      45

```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Thyroid

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 11..171

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93

region 1..161

id HUM085F04B

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 9..109

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98

region 1..101

id AA143653

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: complement(62..155)

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95

region 24..117

id H17554

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 103..185

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90

region 139..221

id H18908

est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 109..185

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93

region 133..209

id H85714

est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 11..154

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.6

seq LLLSFVWMPALLP/DG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

AAACCGCGCC ATG ATA GGG TCG GGA TTG.GCT GGC TCT GGA GGC GCA GGT      49
      Met Ile Gly Ser Gly Leu Ala Gly Ser Gly Gly Ala Gly
                -45                      -40

GGT CCT TCT TCT ACT GTC ACA TGG TGC GCG CTG WTT TCT AAT CAC GTG      97
Gly Pro Ser Ser Thr Val Thr Trp Cys Ala Leu Xaa Ser Asn His Val
-35                -30                      -25                      -20

GCT GCC ACC CAG GCC TCT CTG CTC CTG TCT TTT GTT TGG ATG CCG GCG      145
Ala Ala Thr Gln Ala Ser Leu Leu Leu Ser Phe Val Trp Met Pro Ala
                -15                      -10                      -5

CTG CTG CCT GAT GGC CTC CCG CCW TTT GTT GCT ACC CCG ATG      187
Leu Leu Pro Asp Gly Leu Pro Pro Phe Val Ala Thr Pro Met
                1                5                10

```

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 2..137
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 202..319
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..422
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 316..406
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 167..284
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..153
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..415
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 281..364
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 149..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..137
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 2..133
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..296
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 213..292
id W25483

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 25..148
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 148..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..182
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 307..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..165
id T47061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 217..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 177..294
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 329..369
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 288..328
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 313..366
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LXGFLFXVIVLTS/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

AATAACTGAA AGTAGCTAAG GCACCCCAGC CGGAGGAAGT GAGCTCTCCT GGGGCGTGTT 60
TGTTTCGTGAT CCTTGCATCT GTTACTTAGG GTCAAGGCTT GGGTCTTGCC CCGCAGACCC 120
TTGGGACGAC CCGGCCCCAG CGCASTATGA ACCTGGAGCG AGTGTCCAAT GAGGAGAAAT 180
TGAACCTGTG CCGGAAGTAC TACCTGGGGG GGTTTGCTTT CCTGCCTTTT CTCTGGTTGG 240
TCAACATCTT CTGGTTCTTC CGAGAGGCCT TCCTTGTCCT AGCCTACACA GAACAGAGCC 300
AAATCAAAGG CT ATG TCT GGC GCT CAG CTK HTG GGC TTC CTC TTC TGS GTG 351
Met Ser Gly Ala Gln Leu Xaa Gly Phe Leu Phe Xaa Val
-15 -10
ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC CGC 399
Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro Arg
-5 1 5 10
TGG GGG TGC CCT TGG GGA CTA CCT CTC CTT CAC ATA CCC CTG GGC ACC 447
Trp Gly Cys Pro Trp Gly Leu Pro Leu Leu His Ile Pro Leu Gly Thr
15 20 25
CCT GAC AAC TTC TGC ACA TAC 468
Pro Asp Asn Phe Cys Thr Tyr
30

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: 328..432
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 15..119
id HUMGS01778
est

(ix) FEATURE:

- (A) NAME/KEY: other
(B) LOCATION: complement(256..309)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 175..228
id HSAAAAJHX
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: 188..274
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq VVFMTVAASGASS/FA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

ACGGTTCCGG GCGTTACCAT CGTCCGTGCG CACCGCCCGG CGTCCAGGTG AGTCTCCCAT   60
CTGCAGAGAC GCGGACGCGC CGGCCCGCAG TTGGCCTGCG GACGCGGTGG ACGGTTTGGC  120
GCCCCACCAGG CGATCAATAC TTTGGATTTT TAATTTCTAG ATTTGGCAAT TCTTCGCTGA  180
AGTCATC ATG AGC TTT TTC CAA CTC CTG ATG AAA AGG AAG GAA CTC ATT   229
Met Ser Phe Phe Gln Leu Leu Met Lys Arg Lys Glu Leu Ile
-25 -20

CCC TTG GTG GTG TTC ATG ACT GTG GCG GCG AGT GGA GCC TCA TCT TTC   277
Pro Leu Val Val Phe Met Thr Val Ala Ala Ser Gly Ala Ser Ser Phe
-15 -10 -5 1

GCT GTG TAT TCT CTT TGG AAA ACC GAT GTG ATC CTT GAT CGA AAA AAA   325
Ala Val Tyr Ser Leu Trp Lys Thr Asp Val Ile Leu Asp Arg Lys Lys
5 10 15

AAT CCA GAA CCT TGG GAA ACT GTG GAC CCT ACT GTA CCT CAA AAG CTT   373
Asn Pro Glu Pro Trp Glu Thr Val Asp Pro Thr Val Pro Gln Lys Leu
20 25 30

ATA ACA ATC AAC CAA CAA TGG AAA CCC ATT GAA GAG TTG CAA AAT GTC   421
Ile Thr Ile Asn Gln Gln Trp Lys Pro Ile Glu Glu Leu Gln Asn Val
35 40 45

CAA AGG GTA ACG   433
Gln Arg Val Thr
50

```

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(28..242)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..215
id N91097
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 103..147
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LAHSLLLNNEEALA/QI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```

GCGGGAGGTG GGGCATCCGG GTCTCTTGGT GGCTGCTTCT ACCCCCGGAG CTCAGCTGAT    60
CTTCCCTTCC AGACTACGAG GTGTGAATTT CAAACTTCCG TA ATG GAG TTA GCC    114
                               Met Glu Leu Ala
                               -15
CAC AGT TTA TTG CTA AAT GAA GAA GCT TTG GCT CAA ATC ACC GAA GCA    162
His Ser Leu Leu Leu Asn Glu Glu Ala Leu Ala Gln Ile Thr Glu Ala
-10                      -5                      1                      5
AAA AGA CCA GTT TTC ATC TTT GAA TGG TTG CGA TTT CTT GAT AAA GTC    210
Lys Arg Pro Val Phe Ile Phe Glu Trp Leu Arg Phe Leu Asp Lys Val
                      10                      15                      20
TTG GTT GCT GCC AAC AAG ACC GAT GTA AAG GAA AAA CAG AAA AAA CTT    258
Leu Val Ala Ala Asn Lys Thr Asp Val Lys Glu Lys Gln Lys Lys Leu
                      25                      30                      35
GTT GAA CAA TTA ACT GGA TTA ATA AGT AGT TCA CCT GGA CCC ACC GGG    306
Val Glu Gln Leu Thr Gly Leu Ile Ser Ser Ser Pro Gly Pro Thr Gly
                      40                      45                      50

```

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 6..322
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 15..331
 id H23844
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 11..322
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 21..332
 id H22656
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 12..310
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 8..306
 id AA036876
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 22..204
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..183
 id W05714
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 205..305
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 183..293
 id W05714
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 40..322

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..283
 id R69117
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 56..139
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.5
 seq LGYLVLSEGAFLA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

CTGAAGCCGG AAGCTACCTA TCTGGTAGGG AGCTCCCCCA GCACCGAAGA CTGCG ATG	58
Met	
ACT TCT GCA CTG ACC CAG GGG CTG GAG CGA ATC CCA GAC CAG CTC GGC	106
Thr Ser Ala Leu Thr Gln Gly Leu Glu Arg Ile Pro Asp Gln Leu Gly	
-25 -20 -15	
TAC CTG GTA CTG AGT GAA GGT GCA GTG CTG GCG TCA TCT GGG GAC CTG	154
Tyr Leu Val Leu Ser Glu Gly Ala Val Leu Ala Ser Ser Gly Asp Leu	
-10 -5 1 5	
GAG AAT GAT GAG CAG GCA GCC AGT GCC ATC TCT GAG CTG GTC AGC ACA	202
Glu Asn Asp Glu Gln Ala Ala Ser Ala Ile Ser Glu Leu Val Ser Thr	
10 15 20	
GCC TGC GGT TTC CGG CTG CAC CGC GGC ATG AAT GTG CCC TTC AAG CGC	250
Ala Cys Gly Phe Arg Leu His Arg Gly Met Asn Val Pro Phe Lys Arg	
25 30 35	
CTG TCT GTG GTC TTT GGA GAA CAC ACA CTG CTG GTG ACG GTG TCA GGA	298
Leu Ser Val Val Phe Gly Glu His Thr Leu Leu Val Thr Val Ser Gly	
40 45 50	
CAG AGG GTG TTT GTG GTG AAG AGG GGG	325
Gln Arg Val Phe Val Val Lys Arg Gly	
55 60	

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..374
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 125..358
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 65..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..119
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 388..452
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 374..438
id N47594
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 131..333
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 113..315
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..137
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 43..120
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 323..374
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 304..355
id AA143062
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 388..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 371..416
id AA143062
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..333
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..317
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 388..434
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 370..416
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 8..46
id HUM172D06B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 45..359
id HUM159G08B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..61
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..47
id HUM159G08B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..355
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 92..316
id N34957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 30..97
id N34957

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 12..104
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq LVGVLFVSVTTG/PW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

```

AGGTCTCCAA G ATG GCG GCC GCC TGG CCG TCT GGT CCG KCT GCT CCG GAG      50
      Met Ala Ala Ala Trp Pro Ser Gly Pro Xaa Ala Pro Glu
      -30                      -25                      -20

GCC GTG ACG GCC AGA CTC GTT GGT GTC CTG TGG TTC GTC TCA GTC ACT      98
Ala Val Thr Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr
      -15                      -10                      -5

ACA GGA CCC TGG GGG GCT GTT GCC ACC TCC GCC GGG GGC GAG GAG TCG      146
Thr Gly Pro Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser
      1                      5                      10

CTT AAG TGC GAG GAC CTC AAA GTG GGA CAA TAT ATT TGT AAA GAT CCA      194
Leu Lys Cys Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro
      15                      20                      25                      30

AAA ATA AAT GAC GCT ACG CAA GAA CCA GTT AAC TGT ACA AAC TAC ACA      242
Lys Ile Asn Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr
      35                      40                      45

GCT CAT GTT TCC TGT TTT CCA GCA CCC AAC ATA ACT TGT AAG GAT NCC      290
Ala His Val Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Xaa
      50                      55                      60

AGT GGC AAT GAA ACA CAT TTT ACT GGG AAC GAA GTT GGT TTT TTC AAG      338
Ser Gly Asn Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys
      65                      70                      75

CCC ATA TCT TGC CGA AAT GTA AAT GGC TAT TCC TAC NNT KAG CAG TNN      386
Pro Ile Ser Cys Arg Asn Val Asn Gly Tyr Ser Tyr Xaa Xaa Gln Xaa
      80                      85                      90

NWT GTC TCT TTT TCT TGG ATG GTT GGG AGC AGA TCG ATT TTA CCT TGG      434
Xaa Val Ser Phe Ser Trp Met Val Gly Ser Arg Ser Ile Leu Pro Trp
      95                      100                      105                      110

ATA CCC TGC TTT GGG TTT GTT      455
Ile Pro Cys Phe Gly Phe Val
      115

```

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 170..201

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 157..188
id AA102919
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 117..155

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

AAGCAGCTGG ATCTCCGGTA ACTGAGACAT AGGGTATAAC TGTGTGTCGCG GCGGAGGAAG 60

TGAGGACGGC GCCAAGGGCC TTCCGGGCCA GTGTTGGATC CCTGTAGTTT GTGAAG ATG 119
Met

GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG GAC GGG CTC CCG CTG GCC 167
Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu Ala
-10 -5 1

GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC CGG 200
Ala Ser Met Gln Glu Asp Glu Gln Ser Gly Arg
5 10 15

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 434 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 121..436

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 57..372

id AA023107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 194..436
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 157..399
id AA102919
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 141..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```
AACCTCAGCG GGAAGCGGAG ACGCAAGCAG CTKGATCTCC GGTAAGTGAG ACATAGGGTA    60
TAACTGTTGT CGCGGCGGAG GAAGTGAGGA CGGCGCCAAG GGCCTTCCGG GCCAGTGTG    120
GATCCCTGTA GTTTGTGAAG ATG GTG TTG CTA ACA ATG ATC GCC CGA GTG GCG    173
                Met Val Leu Leu Thr Met Ile Ala Arg Val Ala
                -10                                -5

GAC GGG CTC CCG CTG GCC GCC TCG ATG CAG GAG GAC GAA CAG TCT GGC    221
Asp Gly Leu Pro Leu Ala Ala Ser Met Gln Glu Asp Glu Gln Ser Gly
      1                      5                      10

CGG GAC CTT CAA CAG TAT CAG AGT CAG GCT AAG CAA CTC TTT CGA AAG    269
Arg Asp Leu Gln Gln Tyr Gln Ser Gln Ala Lys Gln Leu Phe Arg Lys
    15                20                25                30

TTG AAT GAA CAG TCC CCT ACC AGA TGT ACC TTG GAA GCA GGA GCC ATG    317
Leu Asn Glu Gln Ser Pro Thr Arg Cys Thr Leu Glu Ala Gly Ala Met
                35                40                45

ACT TTT CAC TAC ATT ATT GAG CAG GGG GTG TGT TAT TTG GTT TTA TGT    365
Thr Phe His Tyr Ile Ile Glu Gln Gly Val Cys Tyr Leu Val Leu Cys
                50                55                60

GAA GCT GCC TTC CCT AAG AAG TTG GCT TTT GCC TAC CTA GAA GAT TTG    413
Glu Ala Ala Phe Pro Lys Lys Leu Ala Phe Ala Tyr Leu Glu Asp Leu
                65                70                75

CAC TCA GAA TTT GAT GAA CAG    434
His Ser Glu Phe Asp Glu Gln
    80                85
```

(12) INFORMATION FOR SEQ ID NO: 206:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 86..333
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 21..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 7..81
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 363..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 349..378
id AA035208
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..288
id R97144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..94
id R97144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..392
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 63..353
id H64963

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 38..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..58
id H64963
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..392
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 32..322
id W03796
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..356
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 86..340
id N73170
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..95
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 3..81
id N73170
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 117..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.4
seq MMVLSLGIXLASA/SF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
AAGAAGATGA AGGTAAGTAG AAACCGTTGA TGGGACTGAG AAACCAGAGT TAAAACCTCT    60
TTGGAGGCTTC TGAGGACTCA GCTGGAACCA AMCGGGCACA GGTGGAAC ACCATC ATG    119
                                         Met
ACA TCA CAA CCT GTT CCC AAT GAG ACC ATC ATA GTG CTC CCA TCA AAT    167
Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser Asn
      -65                               -60                               -55

GTC ATC AAC TTC TCC CAA GCA GAG AAA CCC GAA CCC ACC AAC CAG GGG    215
Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly
      -50                               -45                               -40
```

CAG GAT AGC CTG AAG AAA CAT CTA CAC GCA GAA ATC AAA GTT ATT GGG	263
Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile Gly	
-35 -30 -25	
ACT ATC CAG ATC TTG TGT GGC ATG ATG GTA TTG AGC TTG GGG ATC AKT	311
Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile Xaa	
-20 -15 -10 -5	
TTG GCA TCT GCT TCC TTC TCT CCA AAT TTT ACC CAA GTG ACT TCT ACA	359
Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser Thr	
1 5 10	
CTG TTG AAC TCT GCT TAC CCA TTC ATA GGA CCC TTT TTT TTT ATC ATC	407
Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Phe Phe Phe Ile Ile	
15 20 25	
TCT GGC TCT CTA TCA ATC	425
Ser Gly Ser Leu Ser Ile	
30	

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Placenta

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..347
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 369..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 346..383
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 379..403
id W81335

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..240
id W03593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 239..347
id W03593
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..274
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..234
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 274..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 233..389
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..202
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..177
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 188..336
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 162..310
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..430
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96

region 325..406
id W81261
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..273
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..233
id AA151036
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..430
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 232..389
id AA151036
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 38..112
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

ATTTTTTTTTT CGAGACCGGA AGTGAGTGAT CGAAAGC ATG GCG TCG GTG GTG TTG	55
Met Ala Ser Val Val Leu	
-25 -20	
GCG CTG AGG ACC CGG ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG	103
Ala Leu Arg Thr Arg Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro	
-15 -10 -5	
GCT ACA GCT CTT GCT GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC	151
Ala Thr Ala Leu Ala Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser	
1 5 10	
TCC AAA AAC CTC GGT GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG	199
Ser Lys Asn Leu Gly Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys	
15 20 25	
AAA ATG GAA GGT CAC TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG	247
Lys Met Glu Gly His Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln	
30 35 40 45	
CGC CAT TTC CGC TGG CAC CCA GGT GCC CAT GTG GGT GTT GGG AAG VNT	295
Arg His Phe Arg Trp His Pro Gly Ala His Val Gly Val Gly Lys Xaa	
50 55 60	
AAA TGT CTG TAT GCC CTG GAA GAG GGG ATA GTC CGC TAC ACT AAG GAG	343
Lys Cys Leu Tyr Ala Leu Glu Glu Gly Ile Val Arg Tyr Thr Lys Glu	
65 70 75	
GTC TAC GTG CCT CAT CCC AGA AAC ACG GAG GCT GTG GRT CTG ATC ACC	391

Val Tyr Val Pro His Pro Arg Asn Thr Glu Ala Val Xaa Leu Ile Thr
80 85 90

AGG CTG HYC AAG GGT GCT GTG CTC TAC AAG ACT TTT GTC ACG TGG TTC 439
Arg Leu Xaa Lys Gly Ala Val Leu Tyr Lys Thr Phe Val Thr Trp Phe
95 100 105

CTG 442
Leu
110

(2) INFORMATION FOR SEQ ID NO: 208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 3..347
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 381..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 376..421
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 352..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 346..383
id W81335
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..257
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..234
id AA156841

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 257..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 233..402
id AA156841
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..233
id AA151036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 232..402
id AA151036
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 16..413
id W69555
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 9..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..177
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 171..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 162..310
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 332..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 325..419
id W81261
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 21..95
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq AVTSLLSPTPATA/LA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```

GGAAGTGAGT GATCGAAAGC ATG GCG TCG GTG GTG TTG GCG CTG AGG ACC CGG      53
      Met Ala Ser Val Val Leu Ala Leu Arg Thr Arg
      -25                               -20               -15

ACA GCC GTT ACA TCC TTG CTA AGC CCC ACT CCG GCT ACA GCT CTT GCT      101
Thr Ala Val Thr Ser Leu Leu Ser Pro Thr Pro Ala Thr Ala Leu Ala
      -10                               -5                   1

GTC AGA TAC GCA TCC AAG AAG TCG GGT GGT AGC TCC AAA AAC CTC GGT      149
Val Arg Tyr Ala Ser Lys Lys Ser Gly Gly Ser Ser Lys Asn Leu Gly
      5                               10                   15

GGA AAG TCA TCA GGC AGA CGC CAA GGC ATT AAG AAA ATG GAA GGT CAC      197
Gly Lys Ser Ser Gly Arg Arg Gln Gly Ile Lys Lys Met Glu Gly His
      20                               25                   30

TAT GTT CAT GCT GGG AAC ATC ATT GCA ACA CAG CGC CAT TTC CGC TGG      245
Tyr Val His Ala Gly Asn Ile Ile Ala Thr Gln Arg His Phe Arg Trp
      35                               40                   45                   50

CAC CCA GGT GCC CAT GTG GGT GTT GGG AAG AAT AAA TGT CTG TAT GCC      293
His Pro Gly Ala His Val Gly Val Gly Lys Asn Lys Cys Leu Tyr Ala
      55                               60                   65

CTG GAA GAG GGG ATA VWC CGC TAC ACT AAG GAG GTC TAC GTG CCT CAT      341
Leu Glu Glu Gly Ile Xaa Arg Tyr Thr Lys Glu Val Tyr Val Pro His
      70                               75                   80

CCC AGA AAC ACA GAG GCT GTG GAT CTG ATC ACC AGG CTG CCC AAG GGT      389
Pro Arg Asn Thr Glu Ala Val Asp Leu Ile Thr Arg Leu Pro Lys Gly
      85                               90                   95

GCT GTG CTC TAC AAG ACT TTT GTC CAC GTG GTT CCT      425
Ala Val Leu Tyr Lys Thr Phe Val His Val Val Pro
      100                               105                   110

```

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 89..321
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 334..391
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 40..88
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..50
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..44
id W68063
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 94..329
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 78..313
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..94
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 32..79
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 15..50
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..36
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 364..393
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 349..378
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 62..313
id AA083574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 296..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 312..345
id AA083574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 106..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 97..320
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 3..90
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 342..399
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 333..390
id AA157676
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 94..329
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 86..321
 id R70112
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 47..94
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 40..87
 id R70112
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 111..281
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.3
 seq AIALATVLFLLIGA/FL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

```

ATGAGTGGCA CTTAAGCGGG CCATGCCATG CAACCTTGGG CGCTGCCAAC CGTGGGCGAG      60
CTCTGGGTGT GCGGGCGGCC TGGCGCGGCG CTCCGCTGTG TCAGCGTGTT ATG ATG      116
                                     Met Met
CCG TCC CGT ACC AAC CTG GCT ACT GGA ATC CCC AGT AGT AAA GTG AAA      164
Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys Val Lys
-55                               -50                               -45                               -40
TAT TCA AGG CTC TCC AGC ACA GAC GAT GGC TAC ATT GAC CTT CAG TTT      212
Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu Gln Phe
-35                               -30                               -25
AAG AAA ACC CCT CCT AAG ATC CCT TAT AAG GCC ATC GCA CTT GCC ACT      260
Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu Ala Thr
-20                               -15                               -10
GTG CTG TTT TTG ATT GGC GCC TTT CTC ATT ATT ATA GGC TCC CTC CTG      308
Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser Leu Leu
-5                               1                               5
CTG TCA GGC TAC ATC AGC AAA GGG GGG GCA GAC CGG GCC GTT CCA GTG      356
Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val Pro Val
10                               15                               20                               25
CTG ATC ATT GGC ATT CTG GTG TTC CTA CCC GGA TTT TAC CAC      398
Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
30                               35

```

(2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..344
id W22200
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..330
id R87595
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..287
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 110..286
id R88526
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..112
id R88526
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 118..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 96..309
id AA031849
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..112
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 91
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 49..289
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 63..114
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..53
id T08643
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 242..286
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5.6
seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
GAAAATTGAA ACTGAGTGGC CCACGATGGG AAGASGGGAA AGCCCAGGGG TACAGGAGGC   60
CTCTGGGTGA AGGCAGAGGC TAACATGAGG TTCGGAGCGA CCTTGGCCGT TGGCCTGACC  120
ATCTTTGTGC TGTCTGTCGT CACTATCATC ATCTGCTTCA CCTGCTCCTG CTGCTGCCTT  180
TACAAGACGT GCCGCCGACC ACGTCCGGTT GTCACCACCA CCACATCCAC CACTGTGGTG   240
C ATG CCC CTT ATC CTC AGC CTC CAA GTG TGC CGC CCA GCT ACC CTG GAC   289
  Met Pro Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
   -15                -10                -5                1

CAA GCT ACC AGG GCT ACC ACA CCA TGC CGC CTC AGC CAG GGA TGC CAG   337
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Ser Gln Gly Cys Gln
      5                10                15

CAG CAC CCT ACN NAC CAG                                           355
Gln His Pro Thr Xaa Gln
      20
```

(2) INFORMATION FOR SEQ ID NO: 211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 49..395

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 12..358
id W22200
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 52..383

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..332
id R87595
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 141..317

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 110..286
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 31..142

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 1..112
id R88526
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 148..361

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 96..309
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 58..142

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 7..91
id AA031849
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 141..395
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 49..303
 id T08643
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 93..144
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 2..53
 id T08643
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 272..316
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 5.6
 seq LILSLQVCRPATL/DQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

```

AGATTGCTT TCTTTTCTC CAAAAGGGGA GGAAATTGAA ACTGAGTGGC CCACGATGGG    60
AAGAGGGGAA AGCCCAGGGG TACAGGAGGC CTCTGGGTGA AGGCAGAGGC TAACATGGGG    120
TTCGGAGCGA CCTTGGCCGT TGGCCTGACC ATCTTTGTGC TGTCTGTCGT CACTATCATC    180
ATCTGCTTCA CTGCTCCTG CTGCTGCCTT TACAAGACGT GCCGCCGACC ACGTCCGGTT    240
GTCACCACCA CCACATCCAC CACTGTGGTG C ATG CCC CTT ATC CTC AGC CTC        292
                               Met Pro Leu Ile Leu Ser Leu
                               -15                               -10

CAA GTG TGC CGC CCA GCT ACC CTG GAC CAA GCT ACC AGG GCT ACC ACA        340
Gln Val Cys Arg Pro Ala Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr
                               -5                               1                               5

CCA TGC CGC CTC AGC CAG GGA TGC CAG CAG CAC CCT ACC CAA TGC AGT        388
Pro Cys Arg Leu Ser Gln Gly Cys Gln Gln His Pro Thr Gln Cys Ser
                               10                               15                               20

ACC CAC CTT GGG                                                    400
Thr His Leu Gly
                               25

```

(2) INFORMATION FOR SEQ ID NO: 212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 152..420
id AA146275
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 175..443

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 95
region 152..420
id AA146400
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 199..402

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.2
seq GVLLLLSSIHFQC/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```
ATTTTCAAG ACCGTACTAG GTAGATGGTC AATTAGAGTT CCCAGGGTTT GAAGCCTGTA    60
ACTGCTGCCG CCGCTCAAGC CCTCCAGAGC ATTGCTACGG CTGCTGCCCT TGTACTACTA    120
CCTCCAAATA CGTTCTTGCT GGTAGTGGCG GCAGCAGGAC CAATTACCTC TTTTGTGCTC    180
TCCCTCGAGA AGCTCCAG ATG GCG TCT TCC GTG GGC AAC GTG GCC GAC AGC      231
          Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser
          -65                                -60

ACA GAA CCA ACG AAA CGT ATG CTT TCC TTC CAA GGG TTA GCT GAG TTG      279
Thr Glu Pro Thr Lys Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu
          -55                                -50                                -45

GCA CAT CGA GAA TAT CAG GCA GGA GAT TTT GAG GCA GCB GAG AGA CAC      327
Ala His Arg Glu Tyr Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His
          -40                                -35                                -30

TGC ATG CAG CTC TGG AGA CAA GAG CCA GAC AAT ACT GGT GTG CTT TTA      375
Cys Met Gln Leu Trp Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu
          -25                                -20                                -15                                -10

TTA CTT TCA TCT ATA CAC TTC CAG TGT CGA AGG CTG GAC AGA TCT GCT      423
Leu Leu Ser Ser Ile His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala
          -5                                1                                5
```

CAC TTT AGC ACT CTG GCA
His Phe Ser Thr Leu Ala
10

441

(2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..237
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..218
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 268..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 248..359
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..65
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..47
id AA134795
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..247
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 43..228
id AA134712
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 243..379
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 225..361
id AA134712
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..65
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..47
id AA134712
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 48..329
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq VILQLQLFLFDVLQ/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

ATTGATAGG CGCCGGGCAG CTGAGCTGGT AGGAGGACCA GACGGGG ATG TTC GGC	56
Met Phe Gly	
TCC GCC CCC CAG CGT CCC GTG GCC ATG ACG ACC GCT CAG AGG GAC TCC	104
Ser Ala Pro Gln Arg Pro Val Ala Met Thr Thr Ala Gln Arg Asp Ser	
-90 -85 -80	
CTG TTG TGG AAG CTC GCG GGG TTG CTG CGG GAG TYY GGG GAT GTG GTC	152
Leu Leu Trp Lys Leu Ala Gly Leu Leu Arg Glu Xaa Gly Asp Val Val	
-75 -70 -65 -60	
CTG TCT GGC TGT AGC ACC CTG AGC CTG CTG ACT CCC ACA CTG CAA CAG	200
Leu Ser Gly Cys Ser Thr Leu Ser Leu Leu Thr Pro Thr Leu Gln Gln	
-55 -50 -45	
CTG AAC CAC GTA TTT GAG CTG CAC CTG GGG CCA TGG GGC CCT GGC CAG	248
Leu Asn His Val Phe Glu Leu His Leu Gly Pro Trp Gly Pro Gly Gln	
-40 -35 -30	
ACA GGC TTT GTG GCT CTG CCC TCC CAT CCT GCC GAC TCC CCT GTT ATT	296
Thr Gly Phe Val Ala Leu Pro Ser His Pro Ala Asp Ser Pro Val Ile	
-25 -20 -15	
CTT CAG CTT CAG TTT CTC TTC GAT GTG CTG CAG AAA ACA CTT TCA CTC	344
Leu Gln Leu Gln Phe Leu Phe Asp Val Leu Gln Lys Thr Leu Ser Leu	
-10 -5 1 5	
AAG CTG GTC CAT GTT GCT GGT CCT GGC CCC ACA	377
Lys Leu Val His Val Ala Gly Pro Gly Pro Thr	
10 15	

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 386 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 61..312
id N23581
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..95
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..77
id N23581
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 310..369
id N23581
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 119..292
id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 290..349
id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 100..156
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 62..118

id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 13..64
id AA088606
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..331)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 234..518
id HSGT511
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..387)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 177..236
id HSGT511
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 73..314
id W89716
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 314..371
id W89716
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 99..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 118..350
id W42358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 330..387
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 350..407
id W42358
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..377
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq LILVGTSKHAVFG/KI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```
AGTACATCCG GCGAGTAGCT GCGGGTCCCG GGTGCTGCTG GTTAGTGTGC TCTGAGGGAG   60
GGTCCGAGCC AGCCGCTGTT TTGCCGAGAG AGCCCCTCAG GCCGTAGTAA GCATTAATA   119
ATG TCT TTC ATC TTT GAG TGG ATC TAC AAT GGC TTC AGC AGT GTG CTC   167
Met Ser Phe Ile Phe Glu Trp Ile Tyr Asn Gly Phe Ser Ser Val Leu
  -85                      -80                      -75
CAG TTC CTA GGA CTG TAC AAG AAA TCT GGA AAA CTT GTA TTC TTA GGT   215
Gln Phe Leu Gly Leu Tyr Lys Lys Ser Gly Lys Leu Val Phe Leu Gly
  -70                      -65                      -60                      -55
TTG GAT AAT GCA GGC AAA ACC ACT CTT CTT CAC ATG CTC AAA GAT GAC   263
Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
          -50                      -45                      -40
AGA TTG GGC CAA CAT GTT CCA ACA CTA CAT CCG ACA TCA GAA GAG CTA   311
Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
          -35                      -30                      -25
ACA ATT GCT GGA ATG ACC TTA CAA CTT TTG ATC TTG GTS GGC ACG AGC   359
Thr Ile Ala Gly Met Thr Leu Gln Leu Leu Ile Leu Val Gly Thr Ser
          -20                      -15                      -10
AAG CAC GTC GCG TTT GGA AAA ATT ATC                               386
Lys His Val Ala Phe Gly Lys Ile Ile
  -5                      1
```

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 74..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 78..183
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 176..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 181..266
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..74
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 4..77
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 262..291
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 268..297
id W42807
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 78..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 54..297
id W44615
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 28..61
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..34
id W44615
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..267
id W69940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 57..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..199
id W16769
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 255..321
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 198..264
id W16769
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..189
id N46069
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 222..290
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 185..253
id N46069
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 196..300
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq WYSTVGLLPPVRA/MS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```
AAAGACGCTC ACGGGCGCGC GGACTATCGG GCGGCTAGGC TCTCTGAGGA GGCTGCCACA    60
GTGAAGCAAC CGTGACAAGT GGTGCCCCGAC CAGGGACCTG AACGAGGAAG GTCTGCCAGA    120
GCAGAGAAAG TGAAACTGAT CAGACGAACT ACGAACCCCT GGACGGGAGA GTCTGCCGGC    180
GGAGAATATA AGGAG ATG GAC AAA CCG TGT GGG TGC CCT CCA GGT GTG TGT    231
          Met Asp Lys Pro Cys Gly Cys Pro Pro Gly Val Cys
          -35              -30              -25
GAC CAT GGA ACG GGA GAC CGG AGG GAT CCA TGG TAT TCA ACC GTG GGC    279
Asp His Gly Thr Gly Asp Arg Arg Asp Pro Trp Tyr Ser Thr Val Gly
          -20              -15              -10
CTG TTA CCT CCA GTA CGA GCC ATG AGC CAG CGG AAT CTG AAT    321
```

Leu Leu Pro Pro Val Arg Ala Met Ser Gln Arg Asn Leu Asn
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 161..327
id H07981
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..211
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..155
id H07981
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 193..355
id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 88..188
id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 9..88

id R59645
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 220..426
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 163..369
id H19239
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 115..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 59..164
id H19239
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 2..51
id H19239
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..209
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..178
id AA096397
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 337..371
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 296..330
id AA096397
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 237..266
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 203..232
id AA096397
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 212..345
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 145..278
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..187
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 59..121
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 68..124
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..57
id W05578
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 25..132
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 5
seq ARALAALVPGVTQ/VD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

AGTTTCCGGT TCGCCTCCGG AGCC ATG GCG GCG GCA CTG AAG TGT CTA CTG	51
Met Ala Ala Ala Leu Lys Cys Leu Leu	
-35 -30	
ACA TTA GGA AGA TGG TSC CCC GGC CTT GGA GTG GCT CCC CAG GCC CGG	99
Thr Leu Gly Arg Trp Cys Pro Gly Leu Gly Val Ala Pro Gln Ala Arg	
-25 -20 -15	
GCG CTC GCC GCC TTA GTA CCC GGA GTG ACC CAG GTA GAT AAC AAG TCC	147
Ala Leu Ala Ala Leu Val Pro Gly Val Thr Gln Val Asp Asn Lys Ser	
-10 -5 1 5	
GGT TTC CTG CAG AAG AGG CCT CAT CGC CAG CAC CCT GGC ATC CTA AAG	195
Gly Phe Leu Gln Lys Arg Pro His Arg Gln His Pro Gly Ile Leu Lys	
10 15 20	
CTG CCG CAC GTG CGG CTG CCA CAG GCA CTG GCT AAC GGT GCC CAG TTA	243
Leu Pro His Val Arg Leu Pro Gln Ala Leu Ala Asn Gly Ala Gln Leu	
25 30 35	
TTG CTA CTT GGG AGC GCT GGG CCC ACT ATG GAG AAT CAG GTG CAA ACA	291
Leu Leu Leu Gly Ser Ala Gly Pro Thr Met Glu Asn Gln Val Gln Thr	
40 45 50	
CTG ACC AGT TAT CTC TGG AGC AGA CAT TTG CCT GTA GAG CCA GAS GAG	339
Leu Thr Ser Tyr Leu Trp Ser Arg His Leu Pro Val Glu Pro Xaa Glu	
55 60 65	

TTG CAA AGA CGG GCT ARG CAT CTT GAG AAA AAA TTC CTG GAA AAC CCA	387
Leu Gln Arg Arg Ala Xaa His Leu Glu Lys Lys Phe Leu Glu Asn Pro	
70 75 80 85	
GAC TTA TCT CAG ACA GAG GAG AAA CTT CGT GGA GCA GGG	426
Asp Leu Ser Gln Thr Glu Glu Lys Leu Arg Gly Ala Gly	
90 95	

(2) INFORMATION FOR SEQ ID NO: 217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..374
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 160..350
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 24..107
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 100..149
id AA045902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..173
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 13..159
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..282
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 170..268
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 281..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 268..363
id H45858
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 22..147
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..267
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 200..283
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..361
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 325..381
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 140..189
id W42908
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 184..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 129..321
id N40684
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 56..173
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..118
 id N40684
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 204..336
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 267..399
 id AA005400
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 58..173
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 120..235
 id AA005400
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 31..336
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.9
 seq TVMSALSVAPSKA/RE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

GAGTGTCTT	GCGCGTGGAT	CCGAGCGACC	ATG	GTG	GCC	CGG	GTG	TGG	TCG	CTG	54	
	Met	Val	Ala	Arg	Val	Trp	Ser	Leu				
			-100							-95		
ATG	AGG	TTC	CTC	ATC	AAG	GGA	AGT	GTG	GCT	GGG	GGC	102
Met	Arg	Phe	Leu	Ile	Lys	Gly	Ser	Val	Ala	Gly	Gly	
			-90								-80	
GTG	TAC	GAC	CAG	GAG	CTG	CTG	GGG	CCC	AGC	GAC	AAG	150
Val	Tyr	Asp	Gln	Glu	Leu	Leu	Gly	Pro	Ser	Asp	Lys	
			-75								-65	
CTA	CAG	AAG	GCT	GGG	GAG	GTG	GTC	CCC	CCC	GCC	ATG	198
Leu	Gln	Lys	Ala	Gly	Glu	Val	Val	Pro	Pro	Ala	Met	
			-60								-50	
CAG	TAC	GTG	TGT	CAG	CAG	ACA	GGC	CTG	CAG	ATA	CCC	246
Gln	Tyr	Val	Cys	Gln	Gln	Thr	Gly	Leu	Gln	Ile	Pro	
			-45								-35	
CCT	CCA	AAG	ATT	TAC	TTT	CCC	ATC	CGT	GAC	TCC	TGG	294
Pro	Pro	Lys	Ile	Tyr	Phe	Pro	Ile	Arg	Asp	Ser	Trp	
			-30								-20	
												-15

ATG ACG GTG ATG TCA GCT CTG TCG GTG GCC CCC TCC AAG GCC CGC GAG 342
Met Thr Val Met Ser Ala Leu Ser Val Ala Pro Ser Lys Ala Arg Glu
 -10 -5 1

TAC TCC AAG GAG GGC TGG GAG TAT GTG AAG GCG CTT GGG 381
Tyr Ser Lys Glu Gly Trp Glu Tyr Val Lys Ala Leu Gly
 5 10 15

(2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 11..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..204
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 185..271
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 302..350
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 289..337
id AA248187
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..338
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 11..341
id T93683
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..313
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..295
id AA015679
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 398..445
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq ELQNLXSLQGSQA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

```
AGTTTGTAGC GGACAACATG GCGGCCTTCA TGCTGGGCTC GCTGCTGCGG ACGTTCAAGC   60
AGATGGTTCC TTCATCAGCT TCAGGCCAAG TTCGAAGTCA CTATGTAGAC TGGAGAATGT  120
GGCGCGATGT GAAGAGACGA AAAATGGCCT ATGAATACGC AGATGAGAGG CTACGTATTA  180
ATTCCTCAG GAAGAATACC ATTTTGCCAA AAATTCTTCA GGATGTGGCT GATGAAGAAA  240
TTGCTDHCCT CCCCCGGGAT AGCTGTCCTG TTAGAATCAG AAATCGGTGT GTTATGACGT  300
CCCGTCCGCG TGGTGTGAAG CGGCGCTGGA GGCTTAGTCG TATAGTCTTC CGTCACTTAG  360
CTGACCATGG GCAACTTTCT GGGATCCAGC GAGCGAC ATG GTA AAT GAG CTC CAG   415
                               Met Val Asn Glu Leu Gln
                               -15

AAC CTA TNG AGC TTG CAG GGA AGC CAA GCT TGC AGT TCC AGC AAG CAA   463
Asn Leu Xaa Ser Leu Gln Gly Ser Gln Ala Cys Ser Ser Ser Lys Gln
-10                -5                1                5

AGA TTT                               469
Arg Phe
```

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 102..220
id T30988
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..92
id T30988
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..225
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 110..213
id T30974
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 13..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..100
id T30974
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 84..202
id HSC0CC031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..74
id HSC0CC031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 122..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 84..202
id HSC0CD031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 39..112
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..74
id HSC0CD031
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..240
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..117
id R56565
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 80..151
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FFFSIQPFLLPCSS/RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```
AACACACTCC CTCTCTCTCT CTTTTTAGCA GCAACATACA AGCCGGCCAT ATTAGAGAGA      60
TGGAAATAAA GCTTCCTTA ATG TTG TAT ATG TCT TTG AAG TAC ATC CGT GCA      112
              Met Leu Tyr Met Ser Leu Lys Tyr Ile Arg Ala
              -20                               -15

TTT TTT TTT AGC ATC CAA CCA TTC CTC CCT TGT AGT TCT CGC CCC CTC      160
Phe Phe Phe Ser Ile Gln Pro Phe Leu Pro Cys Ser Ser Arg Pro Leu
              -10                               -5                               1

AAA TCA CCC TCT CCC GTA GCC CAC CCG ACT AAC ATC TCA GTC TCT GAA      208
Lys Ser Pro Ser Pro Val Ala His Pro Thr Asn Ile Ser Val Ser Glu
              5                               10                               15

AAT GCA CAG AGA TGC CTN NCT ACC TCG CCC TGG      241
Asn Ala Gln Arg Cys Leu Xaa Thr Ser Pro Trp
20                               25                               30
```

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 430 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..411
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 167..398
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 38..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 202..399
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..116
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 73..137
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 213..292

id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 85..133
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..278
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..111
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 65..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..182
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 280..341
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 293..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 180..411
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 273..504
id AA032534
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 107..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 200..261
id AA032534
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 110..346
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq WVIVLTSWITIFQ/IY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```

ACATAACTGA AAGTAGCTAA GGCACCCCAG CCGGAGGAAG TGAGCTCTCC TGGGTCAAGG      60
CTTGGGTCTT GCCCCGCAGA CCCTTGGGAC GACCCGGCCC CAGCGCAST ATG AAC CTG      118
                                     Met Asn Leu

GAG CGA GTG TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC      166
Glu Arg Val Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr
-75                               -70                               -65

CTG GGG GGG TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC      214
Leu Gly Gly Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe
-60                               -55                               -50                               -45

TGG TTC TTC CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC      262
Trp Phe Phe Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser
-40                               -35                               -30

CAA ATC AAA GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG      310
Gln Ile Lys Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp
-25                               -20                               -15

GTG ATA GTG CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC TAC CGG CCC      358
Val Ile Val Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile Tyr Arg Pro
-10                               -5                               1

CGC TGG GGT GCC CTH GGG GAC TAS CTC TCC TTC ACC ATA CCC CTG GGC      406
Arg Trp Gly Ala Leu Gly Asp Xaa Leu Ser Phe Thr Ile Pro Leu Gly
5                               10                               15                               20

ACC CCT GAC AAC TTC TGC ACA TAC                                     430
Thr Pro Asp Asn Phe Cys Thr Tyr
25

```

(2) INFORMATION FOR SEQ ID NO: 221:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Normal prostate
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 167..382
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 144..359
 id T27537
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 27..162
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 2..137
 id T27537
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 162..380
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 89..307
 id AA057488
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 75..172
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 1..98
 id AA057488
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 175..381
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 72..278
 id H10316
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 105..174
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 92
region 1..70
id H10316
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 162..385
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 60..283
id T33282
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 104..162
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..59
id T33282
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 174..396
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 65..287
id R14076
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 112..173
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..62
id R14076
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 122..331
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq LVFVLLFIFVKRQ/IM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

```
AATTGCCTGC CTGAGTCACG TGTCAGGGGG AAGCTGGAAG GCGTCGTTCT CCTTTCCCAG      60
CTCTCCTGCC TGTCCGCCAT GTTTTCAGGC CGGGTCTGGC TTGGTCTTCC CCCGTAAGRA      120
A ATG GCC GGG GAG CTC CAG GGG ACC CAG GCG CCG TCG CTT CGD GGA SCT      169
  Met Ala Gly Glu Leu Gln Gly Thr Gln Ala Pro Ser Leu Arg Gly Xaa
  -70                -65                        -60                -55

GGG CTG ACC AGC CAG GAC AGC GGG GTA AAC CCG AAC AAT TCT GYG CGA      217
Gly Leu Thr Ser Gln Asp Ser Gly Val Asn Pro Asn Asn Ser Xaa Arg
```


-50

-45

-40

GGT	AGG	GAG	GCC	ATG	GCG	TCC	GGC	AGT	AAC	TGG	CTC	TCC	GGG	GTG	AAT	265
Gly	Arg	Glu	Ala	Met	Ala	Ser	Gly	Ser	Asn	Trp	Leu	Ser	Gly	Val	Asn	
			-35					-30					-25			
GTC	GTG	CTG	GTG	ATG	GCC	TAC	GGG	AGC	CTG	GTG	TTT	GTA	CTG	CTA	TTT	313
Val	Val	Leu	Val	Met	Ala	Tyr	Gly	Ser	Leu	Val	Phe	Val	Leu	Leu	Phe	
		-20					-15				-10					
ATT	TTT	GTG	AAG	AGG	CAA	ATC	ATG	CGC	TTT	GCA	ATG	AAA	TCT	CGA	AGG	361
Ile	Phe	Val	Lys	Arg	Gln	Ile	Met	Arg	Phe	Ala	Met	Lys	Ser	Arg	Arg	
	-5					1				5					10	
GGA	CCT	CAT	GTC	CCT	GTR	GGR	NCA	CAA	TGC	CCC	CAA	KGT	TGC	TAC	AAC	409
Gly	Pro	His	Val	Pro	Val	Gly	Xaa	Gln	Cys	Pro	Gln	Xaa	Cys	Tyr	Asn	
				15				20					25			
TAT	CTG	TAT														418
Tyr	Leu	Tyr														

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 91..360
id C17648
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 4..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..104
id C17648
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..262
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 93..262

id W07727
est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 260..362
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 261..363
 id W07727
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 2..56
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 4..58
 id W07727
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 58..88
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 59..89
 id W07727
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 94..251
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 95..252
 id W00492
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 2..58
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 4..60
 id W00492
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 253..311
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 255..313
 id W00492
 est

(ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 308..342
 (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 311..345
id W00492
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 60..362
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 64..366
id N29017
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 8..70
id N29017
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 94..359
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 121..386
id N31560
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 116..283
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
seq FACVPGASPTTLA/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

```
AAACGGAGGC AGGTTGGAGC CGCTGCCGTC GCCATGACCC GCGGTAACCA GCGTGAGCTC      60
GCCCCGCCAGA AGAATATGAA AAAGCAGAGC GACTCGGTTA AGGGAAAGCG CCGAG  ATG      118
                                         Met
ACG GGC TTT CTG CTG CCG CCC GCA AGC AGA GGG ACT CGG AGA TCA TGC      166
Thr Gly Phe Leu Leu Pro Pro Ala Ser Arg Gly Thr Arg Arg Ser Cys
-55                      -50                      -45                      -40
AGC AGA AGC AGA AAA AGG CAA ACG AGA AGA AGG AGG AAC CCA AGT AGC      214
Ser Arg Ser Arg Lys Arg Gln Thr Arg Arg Arg Arg Asn Pro Ser Ser
-35                      -30                      -25
TTT GTG GCT TCG TGT CCA ACC CTC TTG CCC TTC GCC TGT GTG CCT GGA      262
Phe Val Ala Ser Cys Pro Thr Leu Leu Pro Phe Ala Cys Val Pro Gly
-20                      -15                      -10
GCC AGT CCC ACC ACG CTC GCG TTT CCT CCT GTA GTG CTC ACA GGT CCC      310
Ala Ser Pro Thr Thr Leu Ala Phe Pro Pro Val Val Leu Thr Gly Pro
```

-5

1

5

AGC ACC GAT GGC ATT CCC TTT GCC CTG AGT CTG CAG MGG GTC CCT TTT 358
Ser Thr Asp Gly Ile Pro Phe Ala Leu Ser Leu Gln Arg Val Pro Phe
10 15 20 25

GTG 361
Val

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 457 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(230..459)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 565..794
id HSZ78357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..205)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 818..1021
id HSZ78357
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 312..389
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 310..337
id AA052404
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 92..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 62..175
id H75454
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 30..94
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 1..65
 id H75454
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 230..307
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.9
 seq VLCTNQVLITARA/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

```

AACTTCCAAG TTGTAGTGTT GTTGTTTTCA GCCTGCTGCT GCTGCTGCTA TTGCGGCTAG      60
GGGAACCGTC GTGGGGAAGG ATGGTGTGCG AAAAATGTGA AAAGAACTT GGTACTGTTA      120
TCACTCCAGA TACATGGAAA GATGGTGCTA GGAATACCAC AGAAAGTGGT GGAAGAAAGC      180
TGAATGAAAA TAAAGCTTTG RCTTCAAAAA AAGCCAGAAT TGAWCCATA ATG GAA GAA      238
                                   Met Glu Glu
                                   -25

WTA AGT KCT CCA CTT GTA GAA TTT GTA AAA GTT TTG TGC ACC AAC CAG      286
Xaa Ser Xaa Pro Leu Val Glu Phe Val Lys Val Leu Cys Thr Asn Gln
                                   -20                               -15                               -10

GTT CTC ATT ACT GCC AGG GCT GTG CCT ACA AAA AAG GCA TCT GTG CGA      334
Val Leu Ile Thr Ala Arg Ala Val Pro Thr Lys Lys Ala Ser Val Arg
                                   -5                               1                               5

TGT GTG GMA AAA AGG TTT TGG ATA CCA AAA ACT ACA AGC AAA CAT CTG      382
Cys Val Xaa Lys Arg Phe Trp Ile Pro Lys Thr Thr Ser Lys His Leu
   10                               15                               20                               25

TCT AGA TGT ATT GAT GGA ATT TCT GGC TTT CTA AAT GAT TTT ACT TTC      430
Ser Arg Cys Ile Asp Gly Ile Ser Gly Phe Leu Asn Asp Phe Thr Phe
                                   30                               35                               40

TGC CTT GAA TTT TCA AGG CAT AGA TGT      457
Cys Leu Glu Phe Ser Arg His Arg Cys
   45                               50

```

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 119..361
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 6..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..120
id AA242967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..261
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 124..260
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..125
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..125
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..311
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 251..309
id C18969
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 125..367
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 101..343
id N40141
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 24..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..102
id N40141
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 125..329
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 122..326
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..125
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..123
id R78319
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..367)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 112..354
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(73..125)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 353..405
id N27018
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 106..156
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq LXXVVAFWAPGES/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

```
ATTCTTTCTT CGCCAGGCTC TCTGCTGACT CAAGTTCTTC AGTTCACGAT CTTCTAGTTG    60
CAGCGATGAG TGCACGAGTG AGATCAAGAT CCAGAGGAAG AGGAG ATG GTC AGG AGG    117
                                     Met Val Arg Arg
                                     -15

CTM MCG AWT GTG GTT GCA TTC GTG GCT CCC GGT GAA TCT CAG CAA GAG    165
Leu Xaa Xaa Val Val Ala Phe Val Ala Pro Gly Glu Ser Gln Gln Glu
```

-10

-5

1

GAA CCA CCA ACT GAC AAT CAG GAT ATT GAA CCT GGA CAA GAG AGA GAA	213
Glu Pro Pro Thr Asp Asn Gln Asp Ile Glu Pro Gly Gln Glu Arg Glu	
5 10 15	
GGA ACA CCT CCG ATC GAA GAA CGT AAA GTA GAA GGT GAT TGC CAG GAA	261
Gly Thr Pro Pro Ile Glu Glu Arg Lys Val Glu Gly Asp Cys Gln Glu	
20 25 30 35	
ATG GAT CTG GAA AAG ACT CGG AGT GAG CGT GGA GAT GGC TCT GAT GTA	309
Met Asp Leu Glu Lys Thr Arg Ser Glu Arg Gly Asp Gly Ser Asp Val	
40 45 50	
AAA GAG AAG ACT CCA CCT AAT CVT AAG CAT GCT AAG ACT AAA GAA GCA	357
Lys Glu Lys Thr Pro Pro Asn Xaa Lys His Ala Lys Thr Lys Glu Ala	
55 60 65	
GGA GAT GGG CCA TTG	372
Gly Asp Gly Pro Leu	
70	

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 299..454
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 278..433
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 160..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 133..236
id AA100750
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..159
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 1..136
id AA100750
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 9..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..347
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 355..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 348..395
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 400..429
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 394..423
id N68686
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 5..245
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 239..337
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 244..342
id H24263
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 13..123
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq PIVRLLSCPGTVA/KD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

TKTTTTTTTAG CA ATG GCG GTT CCC GGC GTG GGG CTC TTG ACC CGT TTG AAC 51
Met Ala Val Pro Gly Val Gly Leu Leu Thr Arg Leu Asn

	-35	-30	-25	
CTG TGT GCC CGG AGA AGA ACT CGA GTC CAG CGG CCT ATC GTC AGG CTT				99
Leu Cys Ala Arg Arg Arg Thr Arg Val Gln Arg Pro Ile Val Arg Leu				
	-20	-15	-10	
TTG AGT TGC CCA GGA ACT GTG GCC AAA GAC CTT AGG AGA GAC GAG CAG				147
Leu Ser Cys Pro Gly Thr Val Ala Lys Asp Leu Arg Arg Asp Glu Gln				
	-5	1	5	
CCT TCA GGG AGC GTG GAG ACA GGC TTT GAA GAC AAG ATT CCC AAA AGG				195
Pro Ser Gly Ser Val Glu Thr Gly Phe Glu Asp Lys Ile Pro Lys Arg				
	10	15	20	
AGA TTC TCG GAG ATG CAA AAT GAA AGA CGA GAA CAG GCA CAG CGG ACT				243
Arg Phe Ser Glu Met Gln Asn Glu Arg Arg Glu Gln Ala Gln Arg Thr				
	25	30	35	40
GTT TTA ATA CAT TGC CCA GAG AAA ATC AGT GAA AAC AAG TTT CKK AAA				291
Val Leu Ile His Cys Pro Glu Lys Ile Ser Glu Asn Lys Phe Xaa Lys				
	45	50	55	
TAT TTA TCC CAA TTT GGA CCT ATT AAT AAT CAT TTC TTC TAT GAA AGC				339
Tyr Leu Ser Gln Phe Gly Pro Ile Asn Asn His Phe Phe Tyr Glu Ser				
	60	65	70	
TTT GGT CTC TAT GCT GTC GTA GAA TTT TGC CAA AAG GAA AGC ATA GGT				387
Phe Gly Leu Tyr Ala Val Val Glu Phe Cys Gln Lys Glu Ser Ile Gly				
	75	80	85	
TCA CTG CAG AAT GGG ACT CAT ACT CCA AGC ACG GCC ATG GAG ACT GCA				435
Ser Leu Gln Asn Gly Thr His Thr Pro Ser Thr Ala Met Glu Thr Ala				
	90	95	100	
ATT CCA TTC AGA TCA CGT TCT TCA				459
Ile Pro Phe Arg Ser Arg Ser Ser				
	105	110		

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 109..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 43..253
id AA017309

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..124
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 28..59
id AA017309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(126..250)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..125
id T52392
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 21..200
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq LVILSLKSQTLDA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

```
AGTAAGTCCC CCCGCCTCGC ATG ATG GCT GCG GTG CCG CCG GGC CTG GAG CCG    53
      Met Met Ala Ala Val Pro Pro Gly Leu Glu Pro
      -60                               -55                               -50

TGG AAC CGT GTG AGA ATC CCT AAG GCG GGG AAC CGC AGC GCA GTG ACA    101
Trp Asn Arg Val Arg Ile Pro Lys Ala Gly Asn Arg Ser Ala Val Thr
      -45                               -40                               -35

GTG CAG AAC CCC GGC GCG GCC CTT GAC CTT TGC ATT GCA GCT GTA ATT    149
Val Gln Asn Pro Gly Ala Ala Leu Asp Leu Cys Ile Ala Ala Val Ile
      -30                               -25                               -20

AAA GAA TGC CAT CTC GTC ATA CTG TCG CTG AAG AGC CAA ACC TTA GAT    197
Lys Glu Cys His Leu Val Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp
      -15                               -10                               -5

GCA GAA ACA GAT GTG TTA TGT GCA GTC CTT TAC AGC AAT CAC AAC AGA    245
Ala Glu Thr Asp Val Leu Cys Ala Val Leu Tyr Ser Asn His Asn Arg
      1                               5                               10                               15

ATG GGC CGC CAC AAA CCC CAT TTG GCC CTC AAA CAG GTT GAG CAA TGT    293
Met Gly Arg His Lys Pro His Leu Ala Leu Lys Gln Val Glu Gln Cys
      20                               25                               30

TTA AAG CGT TTG ARA AAC ATG AAT TTG GAG GGC GGG                    329
Leu Lys Arg Leu Xaa Asn Met Asn Leu Glu Gly Gly
      35                               40
```

(2) INFORMATION FOR SEQ ID NO: 227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 39..385
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 1..347
 id AA023764
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 146..385
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 145..384
 id C03036
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 11..80
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 2..71
 id C03036
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 39..231
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..193
 id R08519
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 232..302
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 193..263
 id R08519
 est
- (ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 11..109

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.8

seq SLVHLLCQNQVLG/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AAGTGGCAAG ATG GCG TCC CTG GAT CGG GTG AAG GTA CTG GTG TTG GGA	49
Met Ala Ser Leu Asp Arg Val Lys Val Leu Val Leu Gly	
-30 -25	
GAC TCA GGT GTT GGG AAA TCT TCG TTA GTC CAT CTC CTA TGC CAA AAT	97
Asp Ser Gly Val Gly Lys Ser Ser Leu Val His Leu Leu Cys Gln Asn	
-20 -15 -10 -5	
CAA GTG CTG GGA AAT CCA TCA TGG ACT GTG GGC TGC TCA GTG GAT GTC	145
Gln Val Leu Gly Asn Pro Ser Trp Thr Val Gly Cys Ser Val Asp Val	
1 5 10	
AGA GTK CAT GAT TAC AAA GAA GGA ACC CCA GAA GAG AAG ACC TAC TAC	193
Arg Val His Asp Tyr Lys Glu Gly Thr Pro Glu Glu Lys Thr Tyr Tyr	
15 20 25	
ATA GAA TTA TGG GAT GTT GGA GGC TCT GTG GGC AGT GCC AGC AGC GTG	241
Ile Glu Leu Trp Asp Val Gly Gly Ser Val Gly Ser Ala Ser Ser Val	
30 35 40	
AAA AGC ACA AGA GCA GTA TTC TAC AAC TCC GTA AAT GGT ATT ATW NYC	289
Lys Ser Thr Arg Ala Val Phe Tyr Asn Ser Val Asn Gly Ile Ile Xaa	
45 50 55 60	
GTA CAC GAC TTA ACV SAT GGG AAG TCC TCC CAA AAM TTG CGN CGT TGG	337
Val His Asp Leu Thr Xaa Gly Lys Ser Ser Gln Xaa Leu Arg Arg Trp	
65 70 75	
TCA TTG GAA GCT CTC AAC AGG GAT TTG GTG CCA ACT GGA GTC TTG GTG	385
Ser Leu Glu Ala Leu Asn Arg Asp Leu Val Pro Thr Gly Val Leu Val	
80 85 90	

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 30..237

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 12..219

id R19497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 219..253
id R19497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..185
id H75597
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 184..218
id H75597
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..179
id H93398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 236..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 178..212
id H93398
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 98..270
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..173
id HUM030E11B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 1..127
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 118..244
id AA280273
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 50..142
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.8
seq WAFSCGTWLPSRA/EW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```
CGGTCCGCGC CATCAGGCCC GAGATAGCGG CGAGGTCCGC TTTCAGTGT ATG GTT TTC    58
                                         Met Val Phe
                                         -30

CCT GCC AAA CGG TTC TGC TTG GTG CCA TCC ATG GAG GGC GTG CGC TGG    106
Pro Ala Lys Arg Phe Cys Leu Val Pro Ser Met Glu Gly Val Arg Trp
      -25                      -20                      -15

GCC TTT TCC TGC GGC ACT TGG CTG CCG AGC CGA GCC GAA TGG CTG CTK    154
Ala Phe Ser Cys Gly Thr Trp Leu Pro Ser Arg Ala Glu Trp Leu Leu
      -10                      -5                      1

RCA GTG CGA TCG ATT CAG CCC GAG GAG AAG GAG CGC ATT GGC CAG TTC    202
Xaa Val Arg Ser Ile Gln Pro Glu Glu Lys Glu Arg Ile Gly Gln Phe
   5                      10                      15                      20

GTC TTT GCC CGG GAC GCT AAG GCA GCC ATG GCT GGT CGT CTG ATG ATA    250
Val Phe Ala Arg Asp Ala Lys Ala Ala Met Ala Gly Arg Leu Met Ile
      25                      30                      35

AGG AAA TTA GTT GCA GAG AAT CGA                                274
Arg Lys Leu Val Ala Glu Asn Arg
      40
```

(2) INFORMATION FOR SEQ ID NO: 229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surrenals

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 90..208
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 105..223

id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 18..115
id HSC13B041
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 71..189
id T08849
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..99
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..81
id T08849
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..101
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..83
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 90..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 71..139
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 153..208
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 140..190
id H88132
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..208
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 92..189
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..110
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..92
id T33149
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..99
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 158..196
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 141..179
id AA121114
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIMQLGSVLLTRC/PF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

ACTTTCCCAA	G	ATG	GCG	TCG	AAG	ATA	GGT	TCG	AGA	CGG	TGG	ATG	TTG	CAG	50	
	Met	Ala	Ser	Lys	Ile	Gly	Ser	Arg	Arg	Trp	Met	Leu	Gln			
	-25						-20					-15				
CTG	ATC	ATG	CAG	TTG	GGT	TCG	GTG	CTG	CTC	ACA	CGC	TGC	CCC	TTT	TGG	98
Leu	Ile	Met	Gln	Leu	Gly	Ser	Val	Leu	Leu	Thr	Arg	Cys	Pro	Phe	Trp	
	-10						-5					1				
GGC	TGC	TTC	AGC	CAG	CTC	ATG	CTG	TAC	GCT	GAG	AGG	GCT	GAG	GCA	CGC	146
Gly	Cys	Phe	Ser	Gln	Leu	Met	Leu	Tyr	Ala	Glu	Arg	Ala	Glu	Ala	Arg	
	5					10				15						
CGG	AAG	CCC	GAC	ATC	CCA	GTG	CCT	TAC	CTG	TAT	TTC	GAC	ATG	GGG	GCA	194
Arg	Lys	Pro	Asp	Ile	Pro	Val	Pro	Tyr	Leu	Tyr	Phe	Asp	Met	Gly	Ala	
	20				25			30							35	
GCC	GTG	CTG	TGC	GCG	CGG											212
Ala	Val	Leu	Cys	Ala	Arg											
						40										

(2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..293
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 19..272
id W52056
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 128..220
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LAVDSWWLDPGHA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

```
AAGAACTGCG TCTCGCGACC CAGGCGCGGG TTCCCGGAGG ACAGCCACCA AGCGATGCTG      60
CCGCCGCCGT TTCCTGATTG GTTGTGGGTG GCTACCTCTT CGTTCTGATT GGCCGCTAGT     120
GAGCAAG ATG CTG AGC AAG GGT CTG AAG CGG AAA CGG GAG GAG GAG GAG      169
Met Leu Ser Lys Gly Leu Lys Arg Lys Arg Glu Glu Glu Glu
-30 -25 -20
GAG AAG GAA CCT CTG GCA GTC GAC TCC TGG TGG CTA GAT CCT GGC CAC      217
Glu Lys Glu Pro Leu Ala Val Asp Ser Trp Trp Leu Asp Pro Gly His
-15 -10 -5
GCA GCG GTG GCA CAG GCA CCC CCG GCC GTG GCC TCT AGC TCC CTC TTT      265
Ala Ala Val Ala Gln Ala Pro Pro Ala Val Ala Ser Ser Ser Leu Phe
1 5 10 15
GAC CTC TCA GTG CTC AAG CTC CAC CAC AGC CGC GGG      301
Asp Leu Ser Val Leu Lys Leu His His Ser Arg Gly
20 25
```

(2) INFORMATION FOR SEQ ID NO: 231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..282
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 88..277
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 40..93
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 36..89
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 347..381
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 345..379
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 7..41
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..36
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 316..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 313..344
id W02951
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..316
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 279..312
id W02951
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 81..293
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..82
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 292..363
id N40687
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 291..367
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 28..81
id N44828
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 93..381
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 79..367
id R91018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..80
id R91018
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 93..305
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 80..292
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 13..93
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..81
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 305..380
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 291..366
id W19557
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 282..329
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq SLAAPALTLHGHWG/LG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

AAGGAACGAG ATGGCGGTTT TCTGGAGGCT GAGTGCCGTT TCGGGTGCCC TAGGAGGCCG 60
AGCTCTGTTG CTTCGAACTC CAGTGGTCAG AMCCTGCTCA TATCTCAGCA TTTCTTCAGG 120
ACCGACCTAT CCCAGAATGG TGTGGAGTGC AGCACATACA CTTGTCACCG AGCCACCATT 180
CTGGCTCCAA GGCTGCATCT CTCCACTGGA CTAGCGAGAG GGTGTGTCAGT GTTTTGCTCC 240

TGGGTCTGCT TCCGGCTGCT TATTTGAATC CTTGCTCTGC G ATG GAC TAT TCC CTG 296
Met Asp Tyr Ser Leu
-15

GCT GCA GCC CTC ACT CTT CAT GGT CAC TGG GGC CTT GGA CAA GTT GTT 344
Ala Ala Ala Leu Thr Leu His Gly His Trp Gly Leu Gly Gln Val Val
-10 -5 1 5

ACT GAC TAT GTT CAT GGG GAT GCC TTG CAG AAA GCT 380
Thr Asp Tyr Val His Gly Asp Ala Leu Gln Lys Ala
10 15

(2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 138..348
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 128..338
id HUM080D04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..143
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..134
id HUM080D04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 348..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 339..399
id HUM080D04B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 407..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94

region 397..435
id HUM080D04B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 127..263
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 11..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..133
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 263..338
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..387
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 339..378
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 374..403
id H29248
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 123..338
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..143

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..134
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 348..397
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 339..388
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 407..437
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 396..426
id HUM179H02B
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 138..299
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 135..296
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 3..143
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..141
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 292..348
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 290..346
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 402..441
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 407..446
id H73551
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 138..326
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 94..282
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 44..143
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 1..100
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 348..408
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 306..366
 id W68502
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 181..396
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.7
 seq LSLXASYIFGISG/FE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```

AGTTTTTCAGG ARATTTGGAA GCTGCCGCAG TAGTTGGAGT CTAAGGACTC GTGACAATCT   60
TCGGGTGCCC TTCGAGAGAA AAGGGGAGGA TGCCACTGGA GTCATCCTCT TCAATGCCAC   120
TATCCTTCCC ATCTBYBYTD RCCCTCRGTA CCACACAATA CTAACCCTTC CCCTNCTCTG   180
ATG TCT TAC ATC ACC TCC CAG GAG ATG AAG TGT ATT CTT CAC TGG TTT   228
Met Ser Tyr Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe
   -70                               -65                               -60

GCC AAT TGG TCA GGT CCC CAG CGT GAA CGT TTC CTA GAG GAC CTG GTA   276
Ala Asn Trp Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val
   -55                               -50                               -45

GCT AAG GCA GTG CCA GAA AAA TTA CAA CCA HTG CTG GAT AGT CTG GAG   324
Ala Lys Ala Val Pro Glu Lys Leu Gln Pro Xaa Leu Asp Ser Leu Glu
   -40                               -35                               -30                               -25

CAG CTT AGT GTG TCT GGG GCA GAC GAC CAC CTT CTA TCT TTG WGT GCC   372
Gln Leu Ser Val Ser Gly Ala Asp Asp His Leu Leu Ser Leu Xaa Ala
   -20                               -15                               -10

AGC TAC ATC TTT GGG ATC AGT GGT TTC GAG GCT GGG GCT GAG CAG GAG   420
Ser Tyr Ile Phe Gly Ile Ser Gly Phe Glu Ala Gly Ala Glu Gln Glu
   -5                               1                               5

```

CGC AAT GAA TTT GTC AGA CAG TCG
Arg Asn Glu Phe Val Arg Gln Ser
10 15

444

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 6..366
id W31798
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 2..353
id AA056667
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 4..342
id AA131958
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 35..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..334
id H10262
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..406
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 1..330
id W95790
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 200..427
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.7
seq LIVYLWVVSFIAS/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
AAGACGAGGT CATGAATCAT GTGACGGTGG CTTGAGGAGG AACCTGTCTT TAAAGCTGTC    60
CCTGAAGTGA CAGCGGAGAG AACCAGGCAG CCCAGAAACC CCAGGCGTGG AGATTGATCC    120
TGCGAGAGAA GGGGGTTCAT CATGGCGGAT GACCTAAAGC GATTCTTGTA TAAAAAGTTA    180
CCAAGTGTTG AAGGGCTCC ATG CCA TTG TTG TGT CAG ATA GAG ATG GAG TAC    232
          Met Pro Leu Leu Cys Gln Ile Glu Met Glu Tyr
          -75                      -70

CTG TTA TTA AAG TGG CAA ATG ACA ATG CTC CAG AGC ATG CTT TGC GAC    280
Leu Leu Leu Lys Trp Gln Met Thr Met Leu Gln Ser Met Leu Cys Asp
-65                      -60                      -55                      -50

CTG GTT TCT TAT CCA CTT TTG CCC TTG CAA CAG ACC AAG GAA GCA AAC    328
Leu Val Ser Tyr Pro Leu Leu Pro Leu Gln Gln Thr Lys Glu Ala Asn
          -45                      -40                      -35

TTG GAC TTT CCA AAA ATA AAA GTA TCA TCT GTT ACT ATA ACA CCT ACC    376
Leu Asp Phe Pro Lys Ile Lys Val Ser Ser Val Thr Ile Thr Pro Thr
          -30                      -25                      -20

AGG TGG TTC MAT TTA ATC GTT TAC CTT TGG GTG GTG AGT TTC ATA GCC    424
Arg Trp Phe Xaa Leu Ile Val Tyr Leu Trp Val Val Ser Phe Ile Ala
          -15                      -10                      -5

AGC AGC AGT    433
Ser Ser Ser
1
```

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Surrrenals.

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..158
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 39..179
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 139..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 161..261
id C15963
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 17..219
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 22..224
id W07092
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(2..239)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 140..377
id W72958
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 16..255
id W24219
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 16..253
id AA040714
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 45..110
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq SVMGVCLLIPGLA/TA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

```

AAAGGACCCA GAAGTAGGGT TTTGGCCTAG GTAACGGGGC AGAG ATG TGG TTC GAG      56
                                   Met Trp Phe Glu
                                   -20

ATT CTC CCC GGA CTC TCC GTC ATG GGC GTG TGC TTG TTG ATT CCA GGA      104
Ile Leu Pro Gly Leu Ser Val Met Gly Val Cys Leu Leu Ile Pro Gly
-15                               -10                               -5

CTG GCT ACT GCG TAC ATC CAC ARG TTC ACT AAC CGG GGC AAG GAA AAA      152
Leu Ala Thr Ala Tyr Ile His Xaa Phe Thr Asn Arg Gly Lys Glu Lys
1                               5                               10

AGG GTT GCT CAT TTT GGG TAT CAC TGG AGT CTG ATG GAA AGA GAT AGG      200
Arg Val Ala His Phe Gly Tyr His Trp Ser Leu Met Glu Arg Asp Arg
15                               20                               25                               30

CGC ATC TCT GGA GTT GAT CGT TAC TAT GTG TCA AAG GGT CCA GGG      245
Arg Ile Ser Gly Val Asp Arg Tyr Tyr Val Ser Lys Gly Pro Gly
35                               40                               45

```

(2) INFORMATION FOR SEQ ID NO: 235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 162..309
id AA017973
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 181..328
id AA021972
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 204..351
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 181..328
id AA013987
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 168..315
id AA014054
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 204..351
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 184..331
id W80073
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 205..342
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq LLVSLVLRXPAKS/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

```
AGTTTAGCGA CCGGACCCGA AACGGGGAAG TTGTCTTG TGAGAGGTT AGTAAAGCAG   60
CGCGCGCGTC ACCAGAGTCG TTTCTCTTCG GAGTCTTAG TGATCGAGGG TGTGCCCAGG  120
GGGCGGACTT GTTTGCGCCT CCCGTTCCCT CCCAATTTCC AAACGTGTCA CCCC GGCGCC   180
GACGGCCCTG TGCAGGGGAA GCAG ATG GAG TTC AAG CTG GAG GCT CAT CGC   231
          Met Glu Phe Lys Leu Glu Ala His Arg
          -45                               -40

ATC GTC AGC ATC TCT CTG GGC AAG ATC TAC AAC TCG CGG GTC CAG CGC   279
Ile Val Ser Ile Ser Leu Gly Lys Ile Tyr Asn Ser Arg Val Gln Arg
          -35                               -30                               -25

GGC GGC ATC AAG CTG CAT AAG AAC CTC CTG GTC TCG CTG GTG CTG CGC   327
Gly Gly Ile Lys Leu His Lys Asn Leu Leu Val Ser Leu Val Leu Arg
          -20                               -15                               -10

ASG CCC GCC AAG TCT ACC CGA GCG GGG                               354
Xaa Pro Ala Lys Ser Thr Arg Ala Gly
          -5                               1
```

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..215
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..179
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 214..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 179..333
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..399
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 334..363
id AA146876
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..319
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 15..285
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 371..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 338..381
id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 307..336

id AA044109
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..362
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 27..337
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 372..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 347..382
id H21138
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..254
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..216
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 307..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 271..332
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 253..315
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 216..278
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 332..376
id AA150025
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 59..368
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 1..310
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 370..414
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 311..355
id N28828
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 94..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.6
seq IASGLGLXLDCT/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

```
AATCTAGCCC CGCCCCAGGC GAGGGCGCCG CACCCACACC GCGCTGCGCA GTTTTGTTCT    60
GCTCCAGCTG TTCGAAGGTG ATCCAGACGC AAG ATG GCT GTC CTC TCT AAG GAA    114
                               Met Ala Val Leu Ser Lys Glu
                               -95

TAT GGT TTT GTG CTT CTA ACT GGT GCT GCC AGC TTT ATA ATG GTG GCC    162
Tyr Gly Phe Val Leu Leu Thr Gly Ala Ala Ser Phe Ile Met Val Ala
-90                               -85                               -80                               -75

CAC CTA GCC ATC AAT GTT TCC AAG GCC CGC AAG AAG TAC AAA GTG GAG    210
His Leu Ala Ile Asn Val Ser Lys Ala Arg Lys Lys Tyr Lys Val Glu
                               -70                               -65                               -60

TAT CCT ATC ATG TAC AGC ACG GAC CCT GAA AAT GGG CAC ATC TTC AAC    258
Tyr Pro Ile Met Tyr Ser Thr Asp Pro Glu Asn Gly His Ile Phe Asn
                               -55                               -50                               -45

TGC ATT CAG CGA GCC CAC CAG AAC ACG TTG GAA GTG TAT CCT CSC TTC    306
Cys Ile Gln Arg Ala His Gln Asn Thr Leu Glu Val Tyr Pro Xaa Phe
                               -40                               -35                               -30

TTA TTT TTT CTA GCT GTT GGA GGT GTT TAC CAC CCG CGT ATA GCT TCT    354
Leu Phe Phe Leu Ala Val Gly Gly Val Tyr His Pro Arg Ile Ala Ser
                               -25                               -20                               -15

GGC CTG GGC TTG DCN CTG GAT TGT TGG ACG AGT TCT TTA TGC TTA TGG    402
Gly Leu Gly Leu Xaa Leu Asp Cys Trp Thr Ser Ser Leu Cys Leu Trp
-10                               -5                               1                               5

CTA TTA CAC GGG CCG GGG    420
Leu Leu His Gly Pro Gly
                               10
```

(2) INFORMATION FOR SEQ ID NO: 237:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: CDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Brain
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 28..227
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 1..200
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 265..310
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 238..283
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 227..263
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 201..237
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: 352..385
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 94
 region 328..361
 id AA074804
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(259..403)
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 123..272
 id N93600
 est
- (ix) FEATURE:
 (A) NAME/KEY: other
 (B) LOCATION: complement(85..207)

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 325..447
id N93600
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(202..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 117..323
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(116..153)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 375..412
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(167..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 324..359
id AA074748
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(258..408)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 123..273
id N93603
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(208..251)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 280..323
id N93603
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(163..202)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 329..368
id N93603
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(90..125)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 411..446
id N93603
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 272..397
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq RIPS LPGSPVCWA/WP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```

AAAAGGAAAG AGGTYSGGAG CGCTCGCGAG ATCTCGGACC ACCCAACCTG AAAGGTGCTT      60
AGGAAGTTGA AAGGCCCAGA GGAGGCCTCC GGGCAAATGG CCGGAGCTGG ACCGACCATG      120
CTGCTACGAG AAGAGAATGG CTGTTGCAGT CGGCGTCAGA GCAGCTCCAG TGCCGGGGAT      180
TCGGACGGAG ASCGCGAGGA CTCGGCGGCT GAGCGCGCCC GACAGCAGCT AGAGGCGCTG      240
CTCAACAAGA CTATGCGCAT TCGCATGACA G ATG GAC GGA CAC TGG TCG GCT          292
                               Met Asp Gly His Trp Ser Ala
                               -40

GCT TTC TCT GCA CTG ACC GTG ACT GCA ATG TCA TCC TGG GCT CGG CGC          340
Ala Phe Ser Ala Leu Thr Val Thr Ala Met Ser Ser Trp Ala Arg Arg
-35                               -30                               -25                               -20

AGG AGT TCC TCA AGC CGT CGG ATT CCT TCT CTG CCG GGG AGC CCC GTG          388
Arg Ser Ser Ser Ser Arg Arg Ile Pro Ser Leu Pro Gly Ser Pro Val
                               -15                               -10                               -5

TGC TGG GCC TGG CCA TGG                                                  406
Cys Trp Ala Trp Pro Trp
                               1

```

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 56..207

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 20..171
id N41898
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 38..176
id H69272
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 56..103
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq RLLLRFLASVIS/RK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ACTTGACAGG CAGGGAGGGC TAGGCTGTGC ATCCCTCCGC TCGCATTGCA GGGAG ATG	58
Met	
GCT CAG CGA CTT CTT CTG AGG AGG TTC CTG GCC TCT GTC ATC TCC AGG	106
Ala Gln Arg Leu Leu Leu Arg Arg Phe Leu Ala Ser Val Ile Ser Arg	
-15 -10 -5 1	
AAG CCC TCT CAG GGT CAG TGG CCA CCC CTC ACT TCC AGA GCC CTG CAG	154
Lys Pro Ser Gln Gly Gln Trp Pro Pro Leu Thr Ser Arg Ala Leu Gln	
5 10 15	
ACC CCA CAA TGC AGT CCT GGT GGC CTG ACT GTA ACA CCC AAC CCA GCC	202
Thr Pro Gln Cys Ser Pro Gly Gly Leu Thr Val Thr Pro Asn Pro Ala	
20 25 30	
CGG ACG	208
Arg Thr	
35	

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 124..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 103..322
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..135
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 4..115
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..398
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 336..377
id H72703
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..343
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..337
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 357..391
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 351..385
id W68324
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 7..134
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..128
id AA054941
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 191..283
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 185..277
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..191
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 117..184
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 361..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 360..397
id AA054941
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 97..316
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..134
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..108
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..398
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 330..371
id AA128297
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(153..300)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 108..255
id H72704
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(291..343)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 64..116

id H72704
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(101..151)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 259..309
id H72704
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(357..398)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 9..50
id H72704
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 311..385
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq FLLLEVSHLLLI/IN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
AGACGTGTTC TTCCGGTGGC GGASGGCGGA TTAGCCTTCG CGGGGCAAAA TGGAGCTCGA    60
GGCCATGAGC AGATATACCA GCCCAGTGAA CCCAGCTGTC TTCCCCCATC TGACCGTGGT    120
GCTTTTGSCC ATTGGCATGT TCTTCACCGC CTGTTTCTTC GTTTACGAGG TCACCTCTAC    180
CAAGTACACT CGTGATATCT ATAAAGAGCT CCTCATCTCC TTAGTGGCCT CACTCTTCAT    240
GGGCTTTGGA GTCCTCTTCC TGCTGCTCTG GGTGGGCATC TACGTGTGAG CACCCAAGGG    300
TAACAACCAG ATG GCT TCA CTG AAA CCT GCT TTT GTA AAT TAC TTT TTT    349
      Met Ala Ser Leu Lys Pro Ala Phe Val Asn Tyr Phe Phe
      -25                      -20                      -15

TTA CTG TTG CTG GAA GTG TCC CAC CTG CTG CTC ATA ATA AAT GCA GAA    397
Leu Leu Leu Leu Glu Val Ser His Leu Leu Leu Ile Ile Asn Ala Glu
      -10                      -5                      1

GGG
Gly
5
400
```

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..396

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 202..372
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 27..162

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 94
region 2..137
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 158..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 134..190
id N40054
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 15..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 2..133
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 226..305

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 98
region 213..292
id W25483
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 157..214

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 144..201
id W25483
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..157
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..124
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 194..292
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 157..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 125..182
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..387
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 293..354
id C17967
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 226..396
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 167..337
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..162
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..102
id N27721
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 158..214
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 99..155

id N27721
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 50..214
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..165
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 226..377
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 177..328
id T47061
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 156..386
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
seq LFWVIVLTSWITI/FQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```
AAAAACGTCC ATAACTGAAA GTAGCTAAGG CACCCCAGCC GGAGGAAGTG AGCTCTCCTG      60
GGGCGTGTT GTTCGTGATC CTTGCATCTG TTAAGGCTTG GGTCTTGCCC      120
CGCAGACCCT TGGGACGACC CGGCCCCAGC GCAST ATG AAC CTG GAG CGA GTG      173
                               Met Asn Leu Glu Arg Val
                               -75

TCC AAT GAG GAG AAA TTG AAC CTG TGC CGG AAG TAC TAC CTG GGG GGG      221
Ser Asn Glu Glu Lys Leu Asn Leu Cys Arg Lys Tyr Tyr Leu Gly Gly
-70                               -65                               -60

TTT GCT TTC CTG CCT TTT CTC TGG TTG GTC AAC ATC TTC TGG TTC TTC      269
Phe Ala Phe Leu Pro Phe Leu Trp Leu Val Asn Ile Phe Trp Phe Phe
-55                               -50                               -45                               -40

CGA GAG GCC TTC CTT GTC CCA GCC TAC ACA GAA CAG AGC CAA ATC AAA      317
Arg Glu Ala Phe Leu Val Pro Ala Tyr Thr Glu Gln Ser Gln Ile Lys
                               -35                               -30                               -25

GGC TAT GTC TGG CGC TCA GCT GTG GGC TTC CTC TTC TGG GTG ATA GTG      365
Gly Tyr Val Trp Arg Ser Ala Val Gly Phe Leu Phe Trp Val Ile Val
                               -20                               -15                               -10

CTC ACC TCC TGG ATC ACC ATC TTC CAG ATC      395
Leu Thr Ser Trp Ile Thr Ile Phe Gln Ile
-5                               1
```

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 80..115
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 170..205
id AA090974
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..135
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq AVASSFFCASLFS/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```
ATTTTTTCT TGCTCGTGGG CTCGGACGAG TACGGAGCGC CTGCAGGGAC AGCCTGGATA    60
AAGGCTCACT TG ATG GCT CAG TTG GGA GCA GTT GTG GCT GTG GCT TCC AGT    111
           Met Ala Gln Leu Gly Ala Val Val Ala Val Ala Ser Ser
           -20                      -15                      -10

TTC TTT TGT GCA TCT CTC TTC TCA GCT GTG CAC AAG ATA GAA GAG GGA    159
Phe Phe Cys Ala Ser Leu Phe Ser Ala Val His Lys Ile Glu Glu Gly
           -5                      1                      5

CAT ATT GGG GTA TAT TAC AGA GGC GGT GTG    189
His Ile Gly Val Tyr Tyr Arg Gly Gly Val
           10                      15
```

(2) INFORMATION FOR SEQ ID NO: 242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 16..262
id AA044042
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 46..78
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..33
id AA044042
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 6..239
id AA127902
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 93..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..216
id AA056679
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(104..308)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 246..450
id W93399
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 126..308
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..184
id H39528
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 122..196
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 4.4
seq LVFMVPLVGLIHL/GW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

```
GCGAAGGTTG TCGGGATCCG CGGCAGCAGC GGCTGCTTGA GATCTGTTTC TGGGGCCTCT    60
GGCGGTGGCG GCCTGGGGCG GCGCGACGGC TGGTGCGCAG GTACACTGAT GCTGAAGTAC    120
T ATG AGC CTT CGG AAC TTG TGG AGA GAC TAC AAA GTT TTG GTT TTT ATG    169
  Met Ser Leu Arg Asn Leu Trp Arg Asp Tyr Lys Val Leu Val Phe Met
   -25                -20                -15                -10

GTC CCT TTA GTT GGG CTC ATA CAT TTG GGG TGG TAC AGA ATC AAA AGC    217
Val Pro Leu Val Gly Leu Ile His Leu Gly Trp Tyr Arg Ile Lys Ser
          -5                      1                      5

AGC CCT GTT TTC CAA ATA CCT AAA AAC GAC GAC ATT CCT GAG CAA GAT    265
Ser Pro Val Phe Gln Ile Pro Lys Asn Asp Asp Ile Pro Glu Gln Asp
          10                15                20

AGT CTG GGA CTT TCA AAT CTT CAG AAG AGC CAA ATC CAG GGG ATA CTG    313
Ser Leu Gly Leu Ser Asn Leu Gln Lys Ser Gln Ile Gln Gly Ile Leu
   25                30                35
```

(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 57..306
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 33..232
id AA088487
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 341..409
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq VFCLLSIPTPSA/HL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

```
AGTCGTTGCC ATSGATCCTG GGGACGACTG GCTGGTGGAA TCCTTGCCTG TGTAATCGT    60
ACCAGGATTT CTATGCATTC GACCTGTCAG GAGCCACTCG AGTCCTTGAA TGGATTGATG   120
ACAAAGGAGT CTTTGTGCT GGCTATGAAA GCCTGAAAAA GAATGAAATT CTTCATCTGA   180
AATTACCTCT CAGACTTTCT GTAAAGGAAA ACAAGGGCTT ATTCCCAGAA AGAGATTTCA   240
AAGTGCGCCA TGGAGGATTT TCAGACAGGT CTATCTTTGA TCTAAAGCAT GTGCCACATA   300
CCAGGTATGG TCAATTTTGT GATCCAGCCA TCCACACAGG ATG GGA TGG GAT GGC    355
                                   Met Gly Trp Asp Gly
                                   -20

TGC AAA TGC CTG GGG GTA TTC TGC CTC CTC ATC TCC ATT CCC ACC CCC    403
Cys Lys Cys Leu Gly Val Phe Cys Leu Leu Ile Ser Ile Pro Thr Pro
      -15                      -10                      -5

TCA GCA CAC CTG                                                    415
Ser Ala His Leu
      1
```

(2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..451
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 122..417
id AA085629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..144
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 14..114
id AA085629
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 156..259
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 99
region 134..237
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 29..126
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 274..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 254..294
id AA132309
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..144
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 15..112
id H35088
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 156..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 63..252
id HUML11153
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..365
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq ILAHLRLGLIPIHA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

AGAGATTGAA G ATG GCG GCT TCT CAG GCG GTG GAG GAA ATG CGG ACC GCG	50
Met Ala Ala Ser Gln Ala Val Glu Glu Met Arg Thr Ala	
-115	-110
TGG TTC TGG GGG AGT TTG GGG TTC GCA ATG TCC ATA CTA CTG ACT TTC	98
Trp Phe Trp Gly Ser Leu Gly Phe Ala Met Ser Ile Leu Leu Thr Phe	
-105	-100 -95 -90
CCG GTA ACT ATT CCG GTT ATG ATG ATG CCT GGG ACC AGG RMC GGY TTC	146
Pro Val Thr Ile Pro Val Met Met Met Pro Gly Thr Arg Xaa Gly Phe	

	-85	-80	-75	
GAA GRA AGA AWT TTC CGT GTG GAT GTA GTA CAC ATG GAT GAA AAC TCA				194
Glu Xaa Arg Xaa Phe Arg Val Asp Val Val His Met Asp Glu Asn Ser				
	-70	-65	-60	
CTG GAG TTT GAC ATG GTG GGA ATT GAC GCA GCC ATT GCC AAT GCT TTT				242
Leu Glu Phe Asp Met Val Gly Ile Asp Ala Ala Ile Ala Asn Ala Phe				
	-55	-50	-45	
CGA CGA ATT CTG CTA GCT GAG GTG CCA ACT ATG GCT GTG GAG AAG GTC				290
Arg Arg Ile Leu Leu Ala Glu Val Pro Thr Met Ala Val Glu Lys Val				
	-40	-35	-30	
CTG GTG TAC AAT AAT ACA TCC ATT GTT CAG GAT GAG ATT CTT GCT CAC				338
Leu Val Tyr Asn Asn Thr Ser Ile Val Gln Asp Glu Ile Leu Ala His				
	-25	-20	-15	-10
CGT CTG GGG CTC ATT CCC ATT CAT GCT GAT CCC CGT CTT TTT GAG TAT				386
Arg Leu Gly Leu Ile Pro Ile His Ala Asp Pro Arg Leu Phe Glu Tyr				
	-5	1	5	
CGG AAC CAA GGA GAT GAA GAA GGC ACA GAG ATA GAT ACT CTA CAG TTT				434
Arg Asn Gln Gly Asp Glu Glu Gly Thr Glu Ile Asp Thr Leu Gln Phe				
	10	15	20	
CGT CTC CAG GTC AGA TGC ACT CGG				458
Arg Leu Gln Val Arg Cys Thr Arg				
	25	30		

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..188
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 45..172
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 234..316

id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 189..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 172..239
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..64
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..49
id AA156837
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..206
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 236..318
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 222..256
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 207..241
id AA196478
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 61..226
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 44..209
id AA181144
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 252..334
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 90
region 235..317
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 17..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..48
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 225..256
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 209..240
id AA181144
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 185..334
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 169..318
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 61..184
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 46..169
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..64
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 8..50
id AA228369
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 15..219
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..205
id W04828
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 252..334
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 236..318
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 341..380
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 323..362
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 221..256
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 206..241
 id W04828
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 12..242
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.4
 seq FEARIALLP LLQA/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

ATACTGCGAG T ATG GCG GCG TCA AAG GTG AAA CAG GAC ATG CCT CCG CCG	50
Met Ala Ala Ser Lys Val Lys Gln Asp Met Pro Pro Pro	
-75 -70 -65	
GGG GGC TAT GGG CCC ATC GAC TAC AAA CGG AAC TTR CCG CGT CGA GGA	98
Gly Gly Tyr Gly Pro Ile Asp Tyr Lys Arg Asn Leu Pro Arg Arg Gly	
-60 -55 -50	
CTG TCG GGC TAC ACC ATG CTG GCC ATA GGG ATT GGA ACC CTG ATC TAC	146
Leu Ser Gly Tyr Ser Met Leu Ala Ile Gly Ile Gly Thr Leu Ile Tyr	
-45 -40 -35	
GGG CAC TGG AGC ATA ATG AAG TGG AAC CGT GAG CGC AGG CGC CTA CAA	194
Gly His Trp Ser Ile Met Lys Trp Asn Arg Glu Arg Arg Arg Leu Gln	
-30 -25 -20	
ATC GAG GAC TTC GAG GCT CGC ATC GCG CTG TTG CCA CTG TTA CAG GCA	242
Ile Glu Asp Phe Glu Ala Arg Ile Ala Leu Leu Pro Leu Leu Gln Ala	
-15 -10 -5	
GAA ACC GAC CGG ARG ACC TTG CAG ATG CTT CGG GAG AAC CTG GAG GAG	290
Glu Thr Asp Arg Xaa Thr Leu Gln Met Leu Arg Glu Asn Leu Glu Glu	
1 5 10 15	
GAG GCC ATC ATC ATG MAG GAC GTS CYC GAC TGG AAS GTG GGG RAA KVV	338
Glu Ala Ile Ile Met Xaa Asp Val Xaa Asp Trp Xaa Val Gly Xaa Xaa	

20

25

30

GHT GTT CCA CAC AAC CCG CTG GGT GCÇ CCC CTT GAT CGG GGA GCT
Xaa Val Pro His Asn Pro Leu Gly Ala Pro Leu Asp Arg Gly Ala
35 40 45

383

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..271
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 54..267
id AA027968
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 105..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 94..278
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 10..108
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..99
id N90497
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..307
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 21..265
id HSC0SD021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..299

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..259
id T31694
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 116..274
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 61..219
id R38457
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..107
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..53
id R38457
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 273..307
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 219..253
id R38457
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 164..289
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq VLFFGTGWIIIDA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```
AATGCGCGAC TGAGCCGGGT GGATGGTACT GCTGCATCCG GGTGTCTGGA GGCTGTGGCC    60
GTTTTGTTTT CTTGGCTAAA ATCGGGGGGAG TGAGGCGGGC CGGCGCGGCG CGACACCGGG    120
CTCCGGAACC ACTGCACGAC GGGGCTGGAC TGACCTGAAA AAA ATG TCT GGA TTT    175
                                   Met Ser Gly Phe
                                   -40
CTA GAG GGC TTG AGA TGC TCA GAA TGC ATT GAC TGG GGG GAA AAG CGC    223
Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp Trp Gly Glu Lys Arg
-35                               -30                               -25
AAT ACT ATT GCT TCC ATT GCT GCT GGT GTA CTA TTT TTT ACA GGC TGG    271
Asp Thr Ile Ala Ser Ile Ala Ala Gly Val Leu Phe Phe Thr Gly Trp
-20                               -15                               -10
TGG ATT ATC ATA GAT GCA GCT GTT ATT TAT CCC ACC CGG    310
Trp Ile Ile Ile Asp Ala Ala Val Ile Tyr Pro Thr Arg
```

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..386
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 73..358
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..100
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 42..71
id AA133050
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 168..313
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 145..290
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..169
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 47..145
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 339..394
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 319..374
id AA159550

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 10..45
id AA159550
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 225..356
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq LVFLTFLSIPSFV/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```

AAGGTGCTCG TCATGCGCAA TGTGGCGCTG CGGCGGGCGG CAGGGCCTGT GTGTGCTGAG   60
GCGGCTGAGC GGCGGACATG CACACCACAG AGCGTGGCGA TGGAACAGTA ACCGGGCTTG   120
TGAGAGGGCT CTGCAGTATA AACTAGGAGA CAAGATCCAT GGATTCACCG TAAACCAGGT   180
GACATCTGTT CCGGAGCTGT TCCTGACTGC AGTGAAGCTC ACCC ATG ATG ACA CAG   236
                               Met Met Thr Gln
GAG CCA GGT ATT TAC ACC TGG CCA GAG AAA ACA CGA ATA ATC TGT TCA   284
Glu Pro Gly Ile Tyr Thr Trp Pro Glu Lys Thr Arg Ile Ile Cys Ser
-40                               -35                               -30                               -25
GCG TGC AGT TCC GTA CCA CTC CCA TGG ACA GTA CTG GTG TTC CTC ACA   332
Ala Cys Ser Ser Val Pro Leu Pro Trp Thr Val Leu Val Phe Leu Thr
                               -20                               -15                               -10
TTC TTG AGC ATA CCG TCC TTT GTG GGT CTC AGA AAT ATC CGT GCA GAG   380
Phe Leu Ser Ile Pro Ser Phe Val Gly Leu Arg Asn Ile Arg Ala Glu
                               -5                               1                               5
ACC TTT CTT CAA AAT GTT   398
Thr Phe Leu Gln Asn Val
10

```

(2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(53..194)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 444..585
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(227..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 311..408
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 230..308
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 183..226
id AA161193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(328..406)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 75..153
id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(275..324)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 156..205
id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(408..446)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 33..71

id R06283
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 328..384
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 286..342
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 131..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 89..141
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 283..324
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 242..283
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 42..85
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 1..44
id AA152388
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 351..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 312..367
id AA159107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 408..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 371..403
id AA159107
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 193..225
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 166..198
id AA159107
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(171..324)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 313..466
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(328..406)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 232..310
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(408..446)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 190..228
id AA152366
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 39..80
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.4
seq FLTALLWRGRIPG/RQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

AGCGGAGACG CAGAGTCTTG AGCAGCGCGN CAGGCACC ATG TTC CTG ACT GCG CTC	56
Met Phe Leu Thr Ala Leu	-10
CTC TGG CGC GGC CGC ATT CCC GGC CGT CAG TGG ATC GGG AAG CAC CGG	104
Leu Trp Arg Gly Arg Ile Pro Gly Arg Gln Trp Ile Gly Lys His Arg	-5 1 5
CSG CCG CGG TTC GTG TCG TTG CGC GCC AAG CAG AAC ATG ATC CGC CGC	152
Arg Pro Arg Phe Val Ser Leu Arg Ala Lys Gln Asn Met Ile Arg Arg	10 15 20
CTG GAG ATC GAG GCG GAG AAC CAT TAC TGG CTG AGC ATG CCC TAC ATG	200
Leu Glu Ile Glu Ala Glu Asn His Tyr Trp Leu Ser Met Pro Tyr Met	25 30 35 40
ACC CGG GAG CAG GAG CGC GGC CAC GCC SSG TTG CGC AGG AGG GAG GCC	248
Thr Arg Glu Gln Glu Arg Gly His Ala Xaa Leu Arg Arg Arg Glu Ala	45 50 55

TTC	GAG	GCS	ATA	AAG	GCG	GCC	GCC	ACT	TCC	AAG	TTC	CCC	CCG	CAT	AGA	296
Phe	Glu	Ala	Ile	Lys	Ala	Ala	Ala	Thr	Ser	Lys	Phe	Pro	Pro	His	Arg	
			60					65						70		
TTC	ATT	GCG	GAC	CAG	CTC	GAC	CAT	CTC	AVK	VGT	CAC	CAA	GAA	ATG	GTC	344
Phe	Ile	Ala	Asp	Gln	Leu	Asp	His	Leu	Xaa	Xaa	His	Gln	Glu	Met	Val	
		75					80					85				
CTA	ATC	CTG	AGT	CGT	CAC	CCT	TGG	ATT	TTA	TGG	ATC	ACG	GAG	CTG	ACC	392
Leu	Ile	Leu	Ser	Arg	His	Pro	Trp	Ile	Leu	Trp	Ile	Thr	Glu	Leu	Thr	
		90				95					100					
ATC	TTT	ACC	TGG	TCT	GGA	CTG	AAA	AAC	TGT	AGC	TTG	TGT	GAA	AAT	GAG	440
Ile	Phe	Thr	Trp	Ser	Gly	Leu	Lys	Asn	Cys	Ser	Leu	Cys	Glu	Asn	Glu	
105					110				115						120	
CTT	TGG	ACC	AGT	CTT	TAT											458
Leu	Trp	Thr	Ser	Leu	Tyr											
				125												

(2) INFORMATION FOR SEQ ID NO: 249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..391
id W56872
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 27..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..291
id W31727
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..375
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99

region 1..354
id W16469
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 45..400
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..356
id N31028
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 22..375
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..354
id W16470
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 120..389
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.3
seq TCLTACWTALCCC/CL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

AACTTGCTCT GAGACAGGTG CGGCAAGTCT ACTGCGGGCT GGTCCGGGCT CCTCAGGTTC	60
AGACCCGACC GTTATCCAGT CGGTTTCGTGG AGAGGAGAGG TGSACTTTAC AGGTCCCCG	119
ATG AAC CAA GAG AAC CCT CCA CCA TAT CCA GGC CCT GGT CCA ACG GCC	167
Met Asn Gln Glu Asn Pro Pro Tyr Pro Gly Pro Gly Pro Thr Ala	
-90 -85 -80 -75	
CCA TAC CCA CCT TAT CCA CCA CAA CCA ATG GGT CCA GGA CHT ATG GGG	215
Pro Tyr Pro Pro Tyr Pro Pro Gln Pro Met Gly Pro Gly Xaa Met Gly	
-70 -65 -60	
GGA CCC TAC CCA CCT CCT CAA GGG TAC CCC TAC CAA GGA TAC CCA CAG	263
Gly Pro Tyr Pro Pro Pro Gln Gly Tyr Pro Tyr Gln Gly Tyr Pro Gln	
-55 -50 -45	
TAC GGC TGG CAG GGT GGA CCT CAG GAG CCT CCT AAA ACC ACA GTG TAT	311
Tyr Gly Trp Gln Gly Gly Pro Gln Glu Pro Pro Lys Thr Thr Val Tyr	
-40 -35 -30	
GTG GTA GAA GAC CAA AGA AGA GAT GAG CTA GGA CCA TCC ACC TGC CTC	359
Val Val Glu Asp Gln Arg Arg Asp Glu Leu Gly Pro Ser Thr Cys Leu	
-25 -20 -15	
ACA GCC TGC TGG ACG GCT CTC TGT TGC TGC TGT CTC TGG	398
Thr Ala Cys Trp Thr Ala Leu Cys Cys Cys Cys Leu Trp	
-10 -5 1	

(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 56..332
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..59
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 329..368
id AA022276
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..284
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 44..273
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 274..321
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..57
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..47
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 318..357
id W87295
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 68..331
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..264
id W01758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 329..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 261..300
id W01758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..259
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 50..249
id W57829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 12..58
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..49
id W57829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..214
id HUM417E03B

est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 11..172
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.3
seq LIVWLLVKSFSSES/GI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

```

AAGTTCGCC ATG GCC TCC TTG GAA GTC AGT CGT AGT CCT CGC AGG TCT      49
  Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser
                    -50                      -45

CGG CGG GAG CTG GAA GTG CGC AGT CCA CGA CAG AAC AAA CAT TCG GTG      97
Arg Arg Glu Leu Glu Val Arg Ser Pro Arg Gln Asn Lys His Ser Val
  -40                      -35                      -30

CTT TTA CCT ACC TAC AAC GAG CGC GAR GAA CTG CCG CTC ATC GTG TGG     145
Leu Leu Pro Thr Tyr Asn Glu Arg Glu Glu Leu Pro Leu Ile Val Trp
-25                      -20                      -15                      -10

CTG CTG GTG AAA AGC TTC TCC GAG AGT GGA ATC AAC TAT GAA ATT ATA     193
Leu Leu Val Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile
                    -5                      1                      5

ATC ATA GAT GAT GGA AGC CCA GAT GGA ACA AGG GAT GTT GCT GAA CAG     241
Ile Ile Asp Asp Gly Ser Pro Asp Gly Thr Arg Asp Val Ala Glu Gln
  10                      15                      20

TTG GAG AAG ATC TAT GGG TCA GAC AGA ATT CTT CTA AGA CCA CGA GAG     289
Leu Glu Lys Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu
  25                      30                      35

AAA AAG TTG GGA CTA GGA ACT GCA TAT ATT CAT GGA ATG RAA ACA TGC     337
Lys Lys Leu Gly Leu Gly Thr Ala Tyr Ile His Gly Met Xaa Thr Cys
  40                      45                      50                      55

CAC AGG RAA CTA CAT CAT TAT TAT GGA TGC                             367
His Arg Xaa Leu His His Tyr Tyr Gly Cys
                    60                      65

```

(2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..408
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 61..399
id AA114853
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 19..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 11..60
id AA114853
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..402
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..391
id W23545
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 42..381
id AA069652
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..68
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..41
id AA069652
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 18..343
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 8..333
id AA084987
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..409
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..347
id AA101916
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 303..344
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq CPTCLCAPSXXWG/EP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```
ATCCGGTGCA CGCGAGTSTT CTGAAACGTC AGCTGCGCTC CCCTAGGAGT GCTGAGCCCCG    60
CGGAACCGCA GCCATGACTG AGGCTGATGT GAATCCAAAG GYCTATCCCC TTGCCGATGC    120
CCACCTCACC AAGAAGCTAC TGGACCTCGT TCAGCAGTCA TGTA ACTATA AGCAGCTTCG    180
GAAAGGWGCC AATGAGGCCA CCAA AACCT CAACAGGGGC ATCTCTGAGT TCATCGTGAT    240
GGCTGCAGAC GCCGAGCCAC TGGAGATCAT TCTGCACCTG CCGCTGCTGT GTGAAGACAA    300
GA ATG TGC CCT ACG TGT TTG TGC GCT CCA AGC AVN SCC TGG GGA GAG    347
  Met Cys Pro Thr Cys Leu Cys Ala Pro Ser Xaa Xaa Trp Gly Glu
                    -10                      -5                      1

CCT GTG GGG TCT CCA GGC CTG TCA TCG CCT GTT CTG TCA CCA TCA AAG    395
Pro Val Gly Ser Pro Gly Leu Ser Ser Pro Val Leu Ser Pro Ser Lys
                    5                      10                      15

AAG GCT CGC AGC
Lys Ala Arg Ser
                    20

                                         407
```

(2) INFORMATION FOR SEQ ID NO: 252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 43..168
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 34..159
id N52621
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 8..38

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..31
id N52621
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..168
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 5..152
id AA157163
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 10..66
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq AVAASAASGQAEG/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```
ACTTCTAAG ATG GCT GCC GCT ACC GGT GCG GTG GCA GCC TCG GCC GCC TCG    51
Met Ala Ala Ala Thr Gly Ala Val Ala Ala Ser Ala Ala Ser
              -15                      -10

GGT CAG GCG GAA GGT AAA AAG ATC ACC GAT CTG CGG GTC ATC GAT CTG    99
Gly Gln Ala Glu Gly Lys Lys Ile Thr Asp Leu Arg Val Ile Asp Leu
-5              1              5              10

AAG TCC GAG CTG AAG CGG CGG AAC TTA GAC ATC ACC GGA GTC AAG ACC    147
Lys Ser Glu Leu Lys Arg Arg Asn Leu Asp Ile Thr Gly Val Lys Thr
              15              20              25

GTG CTC ATC TCC CGA CTA AGG    168
Val Leu Ile Ser Arg Leu Arg
              30
```

(2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..343

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 95..306
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 37..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..103
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 340..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 304..397
id AA102280
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..433
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..388
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R13711
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..401
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 87..356
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..139
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 27..95
id R61022
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 132..389
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 82..339
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 50..139
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 1..90
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 387..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 95
 region 338..384
 id N44705
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 126..433
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 75..382
 id H29689
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 23..73
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.2
 seq SLLXRVSVTAVAA/LS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

ATTCCTCCTG CCCGTAGTAG CC ATG GCG GCC ATG AGT TTG TTG CKG CGG GTT	52
Met Ala Ala Met Ser Leu Leu Xaa Arg Val	
-15 -10	
TCG GTT ACT GCG GTG GCA GCT CTG TCT GGC CGG CCC CTT GGC ACY NGC	100
Ser Val Thr Ala Val Ala Ala Leu Ser Gly Arg Pro Leu Gly Thr Xaa	
-5 1 5	
CTC GGA TTT GGG GGC TTC CTC ACT CGT GGC TTT CCG AAG GCT GCT GCT	148
Leu Gly Phe Gly Gly Phe Leu Thr Arg Gly Phe Pro Lys Ala Ala Ala	
10 15 20 25	
CCT GTT CGA CAC AGT GGA GAC CAT GGG AAA AGA CTA TTT GTC ATC AGA	196
Pro Val Arg His Ser Gly Asp His Gly Lys Arg Leu Phe Val Ile Arg	
30 35 40	

CCT TCT AGA TTC TAT GAC AGG CGT TTT TTG AAG TTA TTG AGA TTC TAC	244
Pro Ser Arg Phe Tyr Asp Arg Arg Phe Leu Lys Leu Leu Arg Phe Tyr	
45 50 55	
ATT GCA TTG ACT GGG ATT CCA GTA GCA WTT TTC ATA ACT CTG GTG AAT	292
Ile Ala Leu Thr Gly Ile Pro Val Ala Xaa Phe Ile Thr Leu Val Asn	
60 65 70	
GTA TTC ATT GGT CAA GCT GAA CTA GCA GAA ATT CCA GAA GGC TAT GTC	340
Val Phe Ile Gly Gln Ala Glu Leu Ala Glu Ile Pro Glu Gly Tyr Val	
75 80 85	
CCA GAA CAC TGG GAA TAT TAT AAG CAT CCC ATA TCA AGA TGG ATT GCC	388
Pro Glu His Trp Glu Tyr Tyr Lys His Pro Ile Ser Arg Trp Ile Ala	
90 95 100 105	
CGT AAT TTC TAT GAT AGT CCT GMA AAG ATA TAT GAA AGA ACA ATG	433
Arg Asn Phe Tyr Asp Ser Pro Xaa Lys Ile Tyr Glu Arg Thr Met	
110 115 120	

(2) INFORMATION FOR SEQ ID NO: 254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 86..452
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 43..409
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..96
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..54
id W00599
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 108..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 107..404
id AA088577

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..100
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 29..96
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 6..41
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 1..36
id AA088577
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 40..189
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 7..156
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 156..279
id R18030
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 100..261
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 46..207
id H85485
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 61..135
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.2
seq LDLLRGLPRVSLA/NL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

GAGACCACGT GGCCTCCGAG CA3CTCAGGG CGCCCTTGAA AGTTCTTGGA TCTGCGGGTT 60

ATG GCC GGT CCC TTG CAG GGC GGT GGG GCC CGG GCC CTG GAC CTA CTC 108
Met Ala Gly Pro Leu Gln Gly Gly Gly Ala Arg Ala Leu Asp Leu Leu

-25	-20	-15	-10	
CGG GGC CTG CCG CGT GTG AGC CTG GCC AAC TTA AAG CCG AAT CCC GGC Arg Gly Leu Pro Arg Val Ser Leu Ala Asn Leu Lys Pro Asn Pro Gly	-5	1	5	156
TCC AAG AAA CCG GAG AGA AGA CCA AGA GGT CGG AGA AGA GGT AGA AAA Ser Lys Lys Pro Glu Arg Arg Pro Arg Gly Arg Arg Gly Arg Lys	10	15	20	204
TGT GGC AGA GGC CAT AAA GGA GAA AGG CAA AGA GGA ACC CGG CCC CGC Cys Gly Arg Gly His Lys Gly Glu Arg Gln Arg Gly Thr Arg Pro Arg	25	30	35	252
TTG GGC TTT GAG GGA GGC CAG ACT CCA TTT TAC ATC CGA RTC CCA AAA Leu Gly Phe Glu Gly Gly Gln Thr Pro Phe Tyr Ile Arg Xaa Pro Lys	40	45	50	300
TAC GGG TTT AAC GAA GGA CAT AGT TTC AGA CGC CAG TAT AAG CCT TTG Tyr Gly Phe Asn Glu Gly His Ser Phe Arg Arg Gln Tyr Lys Pro Leu	60	65	70	348
AGT CTC AAT AGA CTG CAG TAT CTT ATT GAT TTG GGT CGT GTT GAT CCT Ser Leu Asn Arg Leu Gln Tyr Leu Ile Asp Leu Gly Arg Val Asp Pro	75	80	85	396
AGT CAA CCT ATT GAC TTA ACC CAG CTT GTC AAT GGG AGA GGT GTG ACC Ser Gln Pro Ile Asp Leu Thr Gln Leu Val Asn Gly Arg Gly Val Thr	90	95	100	444
ATC GCG CCG Ile Ala Pro	105			453

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..135
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..103
id T11164
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 133..223
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 102..192
 id T11164
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 18..140
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq GILILWIIRLLFS/KT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

AAAGGAAGCG GCTAACT ATG GCG ACC GCC ACG GAG CAG TGG GTT CTG GTG	50
Met Ala Thr Ala Thr Glu Gln Trp Val Leu Val	
-40 -35	
GAG ATG GTA CAG GCG CTT TAC GAG GCT CCT GCT TAC CAT CTT ATT TTG	98
Glu Met Val Gln Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu	
-30 -25 -20 -15	
GAA GGG ATT CTG ATC CTC TGG ATA ATC AGA CTT CTT TTC TCT AAG ACT	146
Glu Gly Ile Leu Ile Leu Trp Ile Ile Arg Leu Leu Phe Ser Lys Thr	
-10 -5 1	
TAC AAA TTA CAA GAA CGA TCT GAT CTT ACA GTC AAG GAA AAA GAA GAA	194
Tyr Lys Leu Gln Glu Arg Ser Asp Leu Thr Val Lys Glu Lys Glu Glu	
5 10 15	
CTG ATT GAA GAG TGG CAA CCA GAA CCT CTT GTT CCT CCT GTC CCA AAA	242
Leu Ile Glu Glu Trp Gln Pro Glu Pro Leu Val Pro Pro Val Pro Lys	
20 25 30	
GAC CAT CCT GCT CTC AAC TAC AAC ATC GTT TCA GGC CCT CCA AGC CAC	290
Asp His Pro Ala Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Ser His	
35 40 45 50	
AAA ACT GTG GTG AAT GGA AAA GAA TGT ATA AAC TTC GCC TCA TTT AAT	338
Lys Thr Val Val Asn Gly Lys Glu Cys Ile Asn Phe Ala Ser Phe Asn	
55 60 65	
TTT CTT GGA TTG TTG GAT AAC CCT AGG GTT AAG GCA GCA GCT TTA GCA	386
Phe Leu Gly Leu Leu Asp Asn Pro Arg Val Lys Ala Ala Ala Leu Ala	
70 75 80	
TCT CTA AAG AAG TAT GGC GTG GGG ACT TGT GGA CCC TGT	425
Ser Leu Lys Lys Tyr Gly Val Gly Thr Cys Gly Pro Cys	
85 90 95	

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs
 (B) TYPE: NUCLEIC ACID

- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..328
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 124..305
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..123
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 326..385
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..361
id W16517
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..149
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..144
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 147..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 145..274
id H23328
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 276..309
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 275..308
id H23328

est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 147..309
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 146..308
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 73..149
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 69..145
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 5..40
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..36
id H06320
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..182
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 222..258
id T62768
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 162..398
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq QGVLFICFTCARS/FP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

```
AAAACTGAG GCCTGGGAGC AGGAACCTGT AGGCAGCGCT TGAGGGTAGC GGGATAGCAG   60
CTGCAACGCG CGTGGGAGGC GGGGGCTCTG GCGGGAACAA AAATCACAGG ATGTCAGAGG  120
ATGTTTCCCG GGAAGAACTG GGATAAAGGG GTCCCAGCAC C ATG GAG GAC CCG AAC   176
                               Met Glu Asp Pro Asn
                               -75

CCT GAA GAG AAC ATG ADG CAG CAG GAT TCA CCC AAG GAG AGA AGT CCC   224
Pro Glu Glu Asn Met Xaa Gln Gln Asp Ser Pro Lys Glu Arg Ser Pro
      -70                      -60

CAG AGC CCA GGA GGC AAC ATC TGC CAC CTG GGG GCC CCG AAG TGC ACC   272
```

Gln	Ser	Pro	Gly	Gly	Asn	Ile	Cys	His	Leu	Gly	Ala	Pro	Lys	Cys	Thr	
			-55					-50					-45			
CGC	TGC	CTC	ATC	ACC	TTC	GCA	GAT	TCC	AAG	TTS	SAG	GAG	CGT	CAC	ATG	320
Arg	Cys	Leu	Ile	Thr	Phe	Ala	Asp	Ser	Lys	Xaa	Xaa	Glu	Arg	His	Met	
		-40					-35					-30				
AAG	CGG	GAG	CAC	CCA	GCG	GAC	TTC	GTG	GCC	CAG	AAG	CTG	CAG	GGG	GTC	368
Lys	Arg	Glu	His	Pro	Ala	Asp	Phe	Val	Ala	Gln	Lys	Leu	Gln	Gly	Val	
	-25					-20					-15					
CTC	TTC	ATC	TGC	TTC	ACC	TGC	GCC	CGC	TCC	TTC	CCC	TCT				407
Leu	Phe	Ile	Cys	Phe	Thr	Cys	Ala	Arg	Ser	Phe	Pro	Ser				
-10					-5					1						

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(166..452)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 16..302
id AA062591
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..45
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 444..490
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 43..89
id AA158358
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..445

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..45
 id AA158431
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 444..490
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 43..89
 id AA158431
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 65..160
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4.1
 seq RLLSSLLLTMSNN/NP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

```

AAGGATCCTC TACCGGCTTT TCGAGTCAGT GCTGCCGCCG CTGCCCGCGG CTTTGCAGAG      60
CAGG ATG AAT GTG ATA GAC CAC GTG CGG GAC ATG GCG GCC GCG GGG CTG      109
  Met Asn Val Ile Asp His Val Arg Asp Met Ala Ala Ala Gly Leu
      -30                      -25                      -20

CAC TCC AAC GTG CGG CTC CTC AGC AGC TTG TTA CTT ACA ATG AGT AAT      157
His Ser Asn Val Arg Leu Leu Ser Ser Leu Leu Leu Thr Met Ser Asn
      -15                      -10                      -5

AAC AAC CCT GAG TTA TTC TCC CCA CCT CAG AAG TAC CAG CTT TTG GTG      205
Asn Asn Pro Glu Leu Phe Ser Pro Pro Gln Lys Tyr Gln Leu Leu Val
      1                      5                      10                      15

TAT CAT GCA GAT TCT CTC TTT CAT GAT AAG GAA TAT CGG AAT GCT GTG      253
Tyr His Ala Asp Ser Leu Phe His Asp Lys Glu Tyr Arg Asn Ala Val
      20                      25                      30

AGT AAG TAT ACC ATG GCT TTA CAG CAG AAG AAA GCG CTA AGT AAA ACT      301
Ser Lys Tyr Thr Met Ala Leu Gln Gln Lys Lys Ala Leu Ser Lys Thr
      35                      40                      45

TCA AAA GTG AGA CCT TCA ACT GGA AAT TCT GCA TCT ACT CCA CAA AGT      349
Ser Lys Val Arg Pro Ser Thr Gly Asn Ser Ala Ser Thr Pro Gln Ser
      50                      55                      60

CAG TGT CTT CCA TCT GAA ATT GAA GTG AAA TAC AAA ATG GCT GAA TGT      397
Gln Cys Leu Pro Ser Glu Ile Glu Val Lys Tyr Lys Met Ala Glu Cys
      65                      70                      75

TAT ACA ATG CTA AAA CAA GAT AAA GAT GCC ATT GCT ATA CTT GAT GGG      445
Tyr Thr Met Leu Lys Gln Asp Lys Asp Ala Ile Ala Ile Leu Asp Gly
      80                      85                      90                      95

KST CCC TTC AAG ACA AAG AAC TCC CAR AAT AAA CAT GAT GCT GGC      490
Xaa Pro Phe Lys Thr Lys Asn Ser Gln Asn Lys His Asp Ala Gly

```

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..312
id HSC26F061
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 20..260
id W30546
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 97..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 66..252
id H34739
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 125..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.1
seq LVHHCPTWQWATG/EE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

```
AGGGTGCTGC CWKCCGGGTG CTGWTGCGAG TCGGTGGCAG CGAGGACATT TTCTGACTCC 60
CTGGCCCCTG ACACGGCTGC ACTTTCCATC CCGTCGCGGG GCCGGCCGCT ACTCCGGCCC 120
CAGG ATG CAG AAT GTG ATT AAT ACT GTG AAG GGA AAG GCA CTG GAA GTG 169
Met Gln Asn Val Ile Asn Thr Val Lys Gly Lys Ala Leu Glu Val
```

-55

-50

-45

GCT GAG TAC CTG ACC CCG GTC CTC AAG GAA TCA AAG TTT AAG GAA ACA	217
Ala Glu Tyr Leu Thr Pro Val Leu Lys Glu Ser Lys Phe Lys Glu Thr	
-40 -35 -30	
GGT GTA ATT ACC CCA GAA GAG TTT GTG GCA GCT GGA GAT CAC CTA GTC	265
Gly Val Ile Thr Pro Glu Glu Phe Val Ala Ala Gly Asp His Leu Val	
-25 -20 -15	
CAC CAC TGT CCA ACA TGG CAA TGG GCT ACA GGG GAA GAA TTG AAA GTG	313
His His Cys Pro Thr Trp Gln Trp Ala Thr Gly Glu Glu Leu Lys Val	
-10 -5 1 5	
AAG GCA TAC CTA CCA ACA GGC AAA TGG	340
Lys Ala Tyr Leu Pro Thr Gly Lys Trp	
10	

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 89..262
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..428
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 334..402
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 260..321
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..114
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 40..88
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..69
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..44
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 428..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 401..438
id W68068
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 62..285
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..45
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..43
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 401..444
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 401..444
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 314..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 312..345
id AA083574

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 283..313
id AA083574
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 127..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 102..264
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 360..465
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 336..441
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 262..323
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 52..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 28..79
id AA001460
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 78..254
id H72445
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 286..347
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100

region 252..313
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..113
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 32..79
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 34..69
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 1..36
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 382..411
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 349..378
id H72445
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 209..472
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.1
seq CIQRLPWLLLCRG/IT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AGATCCCGCC TGGGGCCGGC TGAGTGGCAC TTAAGCGGGC CATGCCATGC AACCTGGGGC	60
GCTGCCAACCC GTGGGCGAGC TCTGGGTGTG CGGGCGGCCT GGCGCGGCGC TCCGCTGTGT	120
CAGCGTGTTA TGATGCCGTC CCGTACCAAC CTGGCTACTG GAATCCCCAG TAGTAAAGTG	180
AAATATTCAA GGCTCTCCAG CACAGACG ATG GCT ACA TTG ACC TTC AGT TTA	232
Met Ala Thr Leu Thr Phe Ser Leu	
-85	
AGA AAA CCC CTC CAA AGA TCC CTT ATA AGG CCA TCG CAC TTG CCA CTG	280
Arg Lys Pro Leu Gln Arg Ser Leu Ile Arg Pro Ser His Leu Pro Leu	
-80 -75 -70 -65	
TGC TGT TTT GAT TGG CGC CTT TCT CAT TAT TAT AGG CTC CCT CCT GCT	328
Cys Cys Phe Asp Trp Arg Leu Ser His Tyr Tyr Arg Leu Pro Pro Ala	
-60 -55 -50	
GTC AGG CTA CAT CAG CAA AGG GGG GGC AGA CCG GGC CGT TCC AGT GCT	376
Val Arg Leu His Gln Gln Arg Gly Gly Arg Pro Gly Arg Ser Ser Ala	

-45

-40

-35

GAT CAT TGG CAT TCT GGT GTT CCT ACC CGG ATT TTA CCA CCT GCG CAT 424
Asp His Trp His Ser Gly Val Pro Thr Arg Ile Leu Pro Pro Ala His
-30 -25 -20

CGC TTA CTA TGC ATC CAA AGG CTA CCG TGG TTA CTC CTA TGC AGG GGG 472
Arg Leu Leu Cys Ile Gln Arg Leu Pro Trp Leu Leu Leu Cys Arg Gly
-15 -10 -5

ATC ACT AGT 481
Ile Thr Ser
1

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 67..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 51..202
id N55991
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..59
id N55991
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 89..231
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..143
id R57473
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 232..339
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 143..250
id R57473
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..243
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 195..298
id H79944
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 243..279
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 299..335
id H79944
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..237
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 97..194
id H70394
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 235..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 193..233
id H70394
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 140..325
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 80..265
id W31972
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 123..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq PSLAAGLLFGSXA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

AAATCGCGTT TCCSGAGAGA CCTGGCTGCT GTGTCCCGCG GCTTGCCTC CGTAGTGGAC 60

```

TCCGCGGGGCC TTCGGCAGAT GCAGGCCTGG GGTAGTCTCC TTTCTGGACT GAGAAGAGAA 120
GA ATG GAG AAG CCC CTC TTC CCA TTA GTG CCT TTG CAT TGG TTT GGC 167
  Met Glu Lys Pro Leu Phe Pro Leu Val Pro Leu His Trp Phe Gly
      -45                      -40                      -35

TTT GGC TAC ACA GCA CTG GTT GTT TCT GGT GGG ATC GTT GGC TAT GTA 215
Phe Gly Tyr Thr Ala Leu Val Val Ser Gly Gly Ile Val Gly Tyr Val
      -30                      -25                      -20

AAA ACA GGC AGC GTG CCG TCC CTG GCT GCA GGG CTG CTC TTC GGC AGT 263
Lys Thr Gly Ser Val Pro Ser Leu Ala Ala Gly Leu Leu Phe Gly Ser
      -15                      -10                      -5

VWA GCC GGC CTG GGT GCT TAC CAG CTG TAT CAG GAT CCA AGR AAC GTT 311
Xaa Ala Gly Leu Gly Ala Tyr Gln Leu Tyr Gln Asp Pro Arg Asn Val
      1                      5                      10

TGG GGT TTC CTA GCC GCT ACA TCT GTT 338
Trp Gly Phe Leu Ala Ala Thr Ser Val
      15                      20

```

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 95..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 92..238
id R27748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..90
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..89
id R27748
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 162..298
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 116..252
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 2..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 11..56
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 61..98
id T79527
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 95..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 59..159
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 194..241
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 159..206
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..90
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 14..56
id R08734
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 102..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 32..228
id H35655
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 102..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: .identity 90
region 108..304
id AA038389
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 108..161
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq VAVGLTIAAAGFA/GR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

```
AGGGGGTTGC GTCGCTCTCT GGTAAGGCG TGCAGGTGTT GGCCGCGGCC TCTGAGCTGG      60
GATGAGCCGT GCTCCCGGTG GAAGCAAGGG GAGCCCCAGC SGGAGCC ATG GCC AGT      116
                               Met Ala Ser
ACA GTG GTA GCA GTT GGA CTG ACC ATT GCT GCT GCA GGA TTT GCA GGC      164
Thr Val Val Ala Val Gly Leu Thr Ile Ala Ala Ala Gly Phe Ala Gly
-15                -10                -5                1
CGT TAC GTT TTG CAA GCC ATG AAG CAT ATG GAG CBT CAA GTA AAA CAA      212
Arg Tyr Val Leu Gln Ala Met Lys His Met Glu Xaa Gln Val Lys Gln
                    5                10                15
GTT TTT CAA AGC CTA CCA AAA TCT GCC TTC AGT GGT GGC TAT TAT AGA      260
Val Phe Gln Ser Leu Pro Lys Ser Ala Phe Ser Gly Gly Tyr Tyr Arg
                20                25                30
GGT BGG TTT GAA CCC ARA ATG RCA AAA CGG GAA GCA GCG GGG      302
Gly Xaa Phe Glu Pro Xaa Met Xaa Lys Arg Glu Ala Ala Gly
    35                40                45
```

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..311
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 96..277
id T32007

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..98
id T32007
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R19207
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..78
id R36562
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 130..314
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 76..260
id R59039
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 19..78
id R59039
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 130..314
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 70..254
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..72
id T35666
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 136..384
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4
seq AFSFSRLLSQCRP/DC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

```
AAAGTTCTCC TTCCACCTTC CCCCACCCTT CTCTGCCAAC CGCTGTTTCA GCCCCTAGCT    60
GGATTCCAGC CATTGCTGCA GCTGCTCCAC AGCCCTTTTC AGGACCCAAA CAACCGCAGC    120
CGCTGTTCCC CAGGR ATG GTG ATC CGT GTA TAT ATT GCA TCT TCC TCT GGC    171
      Met Val Ile Arg Val Tyr Ile Ala Ser Ser Ser Gly
      -80                               -75

TCT ACA GCG ATT AAG AAG AAA CAA CAA GAT GTG CTT GGT TTC CTA GAA    219
Ser Thr Ala Ile Lys Lys Lys Gln Gln Asp Val Leu Gly Phe Leu Glu
-70                               -65                               -60

GCC AAC AAA ATA GGA TTT GAA GAA AAA GAT ATT GCA GCC AAT GAA GAG    267
Ala Asn Lys Ile Gly Phe Glu Glu Lys Asp Ile Ala Ala Asn Glu Glu
-55                               -50                               -45                               -40

AAT CGG AAG TGG ATG AGA GAA AAT GTA CCT GAA AAT AGT CGA CCA GCG    315
Asn Arg Lys Trp Met Arg Glu Asn Val Pro Glu Asn Ser Arg Pro Ala
-35                               -30                               -25

GTT CAG GGG CCA CAT GCT TTT CGG TAT AAA GCA TTC TCC TTC TCT AGG    363
Val Gln Gly Pro His Ala Phe Arg Tyr Lys Ala Phe Ser Phe Ser Arg
-20                               -15                               -10

TTG CTA TCA CAG TGC AGA CCT GAC TGC CTG AAT ATG CTC AGG AGA TTT    411
Leu Leu Ser Ser Gln Cys Arg Pro Asp Cys Leu Asn Met Leu Arg Arg Phe
-5                               1                               5

AGT CAA TAT TGT CTG TAT TTG GTT ATG GAA AAG GCT CTC CTT TTT TTT    459
```

Ser Gln Tyr Cys Leu Tyr Leu Val Met Glu Lys Ala Leu Leu Phe Phe
10 15 20 25

TTT TTT
Phe Phe

465

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..289
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 117..274
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..116
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 315..368
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 302..355
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..316
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 270..302
id R14800
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 132..330

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 113..311
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 36..112
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..41
id R59757
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 132..330
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 94..292
id R25047
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 54..130
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 17..93
id R25047
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 59..352
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 38..331
id R23993
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 163..294
id W23811
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 132..194
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 131..193
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 305..354
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 308..357
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 350..390
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 354..394
 id W23811
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 243..368
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 4
 seq ITSSLFLGRGSA/SN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

```

AAGAAGCCGG TGGCCGCGCA GGAGGACGGA GCCCTAACCG CAACCCGCGC CGCGCCGCGC   60
CGATTTGATT TGTATCCACT GTCACCAGCA CTGCTCACTT AGGACTTTCT GGATCCAGAC   120
CCAGGCAGCG CACACTGGAC TCTTGAGGAA GAAGGAGACT CTAATTTTGG ATTCCTTGGT   180
GGAGGAAAAT AAAACACTCT GGTCTTGCCG CCAACGATGC AAGTGTGACT GCTGGCGTCT   240
TC ATG AGC TCC AGA GGT CAC AGC ACG CTA CCA AGG ACT CTC ATG GCC   287
  Met Ser Ser Arg Gly His Ser Thr Leu Pro Arg Thr Leu Met Ala
    -40                      -35                      -30

CCT CGG ATG ATT TCC GAG GGA GAC ATA GGA GGC ATT GCT CAA ATC ACC   335
Pro Arg Met Ile Ser Glu Gly Asp Ile Gly Gly Ile Ala Gln Ile Thr
   -25                      -20                      -15

TCC TCT CTA TTC CTG GGC AGA GGC AGT GTG GCC TCC AAT CGG CAC CTC   383
Ser Ser Leu Phe Leu Gly Arg Gly Ser Val Ala Ser Asn Arg His Leu
   -10                      -5                      1                      5

CTC CAG GCT CGT GGC ATC   401
Leu Gln Ala Arg Gly Ile
      10

```

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Dystrophic muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..228
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 2..183
id AA022583
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(69..228)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 281..440
id AA022584
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 66..119
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq PALCLFDVDGTLT/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

```

AGGAAGTTCC GGGCCGAGTT CCTCGTGCCA ACGTGTCTTG TAAGGTGCGG CTAGAAACTG      60
GGGAC ATG GCA GCG CCT GGC CCA GCG CTC TGC CTC TTC GAC GTG GAT GGG      110
    Met Ala Ala Pro Gly Pro Ala Leu Cys Leu Phe Asp Val Asp Gly
          -15                      -10                      -5

ACC CTC ACC GCC CCG CGG CAG AAA ATT ACC AAA GAA ATG GAT GAC TTC      158
Thr Leu Thr Ala Pro Arg Gln Lys Ile Thr Lys Glu Met Asp Asp Phe
          1                      5                      10

CTA CAA AAA TTG AGG CAG AAG ATC AAA ATC GGA GTG GTA GGC GGA TCG      206
Leu Gln Lys Leu Arg Gln Lys Ile Lys Ile Gly Val Val Gly Gly Ser
          15                      20                      25

GAC TTT GAG AAA GTG CAG GAA CGG      230
Asp Phe Glu Lys Val Gln Glu Arg
          30                      35

```

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..220
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 159..278
id H97758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 107..160
id H97758
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 166..250
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 114..167
id N59486
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 148..201
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 5..54
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..51
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 200..229
id R09724
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 101..178
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 170..247
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 53..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 121..171
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 173..218
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 240..285
id W90369
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..103
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..90
id N56221
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 126..182
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq ILFHGVFYAGGFA/IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

```
ACTGGAAGAA CTCGTCATGC TCTTTGTAGC GTGGTGCTTC TGTTGCTCAC AGGACAACTT   60
GCCTTTGATG ATTTTCAAGA GAGTTGTGCT ATGATGTGGC AAAGTATGCA GGAAGCAGGC   120
GGTCA ATG CCT CTG GGA GCA AGG ATC CTT TTC CAC GGT GTG TTC TAT GCC   170
  Met Pro Leu Gly Ala Arg Ile Leu Phe His Gly Val Phe Tyr Ala
                -15                      -10                      -5

GGG GGC TTT GCC ATT GTG TAT TAC CTC ATT CAA AAG TTT CAT TCC AGG   218
Gly Gly Phe Ala Ile Val Tyr Tyr Leu Ile Gln Lys Phe His Ser Arg
                1                      5                      10

ACA CTG
Thr Leu                                           224
```

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..239
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..216
id HUM429E03B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 235..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 211..303
id HUM429E03B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 124..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 107..310
id T80259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 31..130
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 15..114
id T80259
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..283
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 1..245
id T31768
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 271..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 234..290
id T31768
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 47..272
id N32697
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..97
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..43
id N32697
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 65..327
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..263
id N44613
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 156..194
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq MLLSIGMLMLSAT/QV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

```

GCCTAGGTGT TGTCGTCCCT GCTAGTACTC CGGGCTGTGG GGGTCGGTGC GGATATTCAG   60
TCATGAAATC AGGGTAGGGA CTTCTCCCGC AGCGACGCGG CTGGCAAGAC TGTTTGTGTT   120
GCGGGGGCCG GACTTCAAGG TGATTTTACA ACGAG ATG CTG CTC TCC ATA GGG       173
                               Met Leu Leu Ser Ile Gly
                               -10
ATG CTC ATG CTG TCA GCC ACA CAA GTC TAC ACC ATC TTG ACT GTC CAG       221
Met Leu Met Leu Ser Ala Thr Gln Val Tyr Thr Ile Leu Thr Val Gln
      -5                      1                      5
CTC TTT GCA TTC TTA AAC CTA CTG CCT GTA GAA GYA GAC ATT TTA GCA       269
Leu Phe Ala Phe Leu Asn Leu Leu Pro Val Glu Xaa Asp Ile Leu Ala
  10                      15                      20                      25
TAT AAC TTT GAA AAT GCA TCT CAG ACA TTT GAT GAC CTC CCT GCA AGA       317
Tyr Asn Phe Glu Asn Ala Ser Gln Thr Phe Asp Asp Leu Pro Ala Arg
                30                      35                      40
TTT GGT TAT
Phe Gly Tyr                                           326

```

(2) INFORMATION FOR SEQ ID NO: 267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 28..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..368
id AA150637
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 33..297
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 30..294
id H02768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 181..372
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 148..339
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 33..179
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 1..147
id H70139
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(267..394)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 231..358
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(184..277)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 349..442
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(109..164)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 464..519
id W46236
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 188..366
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 72..250
id N30922
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 117..180
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..64
id N30922
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 111..185
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq WIAAVTIAAGTAA/IG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

```

AATCGCGGAG TCGGTGCTTT AGTACGCCGC TGGCACCTTT ACTCTCGCCG GCCGCGCGAA    60
CCC GTTTGAG CTCGGTATCC TAGTGCACAC GCCTTGCAAG CGACGGCGCC ATG AGT    116
                                   Met Ser
                                   -25

CTG ACT TCC AGT TCC AGC GTA CGA GTT GAA TGG ATC GCA GCA GTT ACC    164
Leu Thr Ser Ser Ser Ser Val Arg Val Glu Trp Ile Ala Ala Val Thr
          -20                      -15                      -10

ATT GCT GCT GGG ACA GCT GCA ATT GGT TAT CTA GCT TAC AAA AGA TTT    212
Ile Ala Ala Gly Thr Ala Ala Ile Gly Tyr Leu Ala Tyr Lys Arg Phe
      -5                      1                      5

TAT GTT AAA GAT CAT CGA AAT AAA GCT ATG ATA AAC CTT CAC ATC CAG    260
Tyr Val Lys Asp His Arg Asn Lys Ala Met Ile Asn Leu His Ile Gln
    10                      15                      20                      25

AAA GAC AAC CCC AAG ATA GTA CAT GCT TTT GAC ATG GAG GAT TTS RNA    308
Lys Asp Asn Pro Lys Ile Val His Ala Phe Asp Met Glu Asp Xaa Xaa
          30                      35                      40

GAT AAA GCT GTG TAC TGC CGT TGT TGG AGG TCC AAA AAG TTC CCA TTC    356
Asp Lys Ala Val Tyr Cys Arg Cys Trp Arg Ser Lys Lys Phe Pro Phe
          45                      50                      55

TGT GAT GGG GCT CAC ACA ARM VAT AAC GAA GAG ACT GGG CTG    398
Cys Asp Gly Ala His Thr Xaa Xaa Asn Glu Glu Thr Gly Leu
          60                      65                      70

```

(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..150
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 31..126
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 151..212
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 126..187
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..35
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 211..242
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 185..216
id AA094226
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..263
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 202..410
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 172..206
id R54574
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 159..280
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 174..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 279..340
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 129..163
id R13710
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 55..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 189..299
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 163..203
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 298..338
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 24..58
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 159..193
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 201..235
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 337..371
id T78111
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 70..252
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq YTAVSVLGPRWA/DP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```

AATTACGCAG AGAGAAAGTT ACGAGAAACT CGTTTTTCATC TTCTTGTTT CATCYTAAAT      60
ACCAACGTC ATG TCT GGT TCT AAT GGT TCC AAA GAA AAT TCT CAC AAT AAG      111
    Met Ser Gly Ser Asn Gly Ser Lys Glu Asn Ser His Asn Lys
        -60                -55                -50

GCT CGG ACG TCT CCT TAC CCA GGT TCA AAA GTT GAA CGA AGC CAG GTT      159
Ala Arg Thr Ser Pro Tyr Pro Gly Ser Lys Val Glu Arg Ser Gln Val
    -45                -40                -35

CCT AAT GAG AAA GTG GGC TGG CTT GTT GAG TGG CAA GAC TAT AAG CCT      207
Pro Asn Glu Lys Val Gly Trp Leu Val Glu Trp Gln Asp Tyr Lys Pro
    -30                -25                -20

GTG GAA TAC ACT GCA GTC TCT GTC TTG GCT GGA CCC AGG TGG GCA GAT      255
Val Glu Tyr Thr Ala Val Ser Val Leu Ala Gly Pro Arg Trp Ala Asp
    -15                -10                -5                1

CCT CAG ATC AGT GAV AGT VAT TTT TCT CCC AAG TTT AAC GAA AAG GAT      303
Pro Gln Ile Ser Xaa Ser Xaa Phe Ser Pro Lys Phe Asn Glu Lys Asp
        5                10                15

GGG CAT GTT GAG AGA NAG AGC AAG AAT GGC CTG TAT GAG ATT GAN AAT      351
Gly His Val Glu Arg Xaa Ser Lys Asn Gly Leu Tyr Glu Ile Xaa Asn
    20                25                30

GGA AGA CCG AGA AAT CCT GCA GAC GGA CTG GAC TGG TGG GCC      393
Gly Arg Pro Arg Asn Pro Ala Asp Gly Leu Asp Trp Trp Ala
    35                40                45

```

(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 137..335
id HSC1QH021
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 154..291
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93

region 126..263
id HUML12288
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..111
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..87
id HUML12288
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 178..443
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..266
id R60742
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 154..303
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 133..232
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 53..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 35..129
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 18..49
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 1..32
id HSC07D011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 154..298
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 136..230
id C04685
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 25..147

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 10..132
id C04685
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 349..438
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.9
seq LWMRWTVTSTTRA/WI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```
AAAACCTTAG CAAGATGGCG GCTCCCTGGG CGTCCCTGCG CCTGGTCGCC CCCATGTGGA    60
ATGGGCGTAT CAGGGGCATC CATCGCCTGG GTGCGGCAGT GGCCCCAGAG GGCAATCAGA   120
AGAAGAAAAG GACAATAMTC CARPTYCCTG GMCCVAASTA TTTCTACGAT GTGGAGGCTC   180
TGAGGGATTA CTTGCTCCAA AGGGAGATGT ACAAGGTGCA TGAGAAAAAT CGATCTTACA   240
CCTGGCTGGA GAAGCAACAT GGTCCATACG GCGCAGGTGC CTTTTTCATC CTGAAGCAGG   300
GAGGCGCAGT CAAGTTTCGA GACAAGGAGT GGATCAGGCC AGATAAGT ATG GCC ATT    357
                               Met Ala Ile
                               -30

TCT CTC AGG AGT TCT GGA ATT TCT GTG AAG TGC CTG TCG AAG CTG TGG    405
Ser Leu Arg Ser Ser Gly Ile Ser Val Lys Cys Leu Ser Lys Leu Trp
      -25                      -20                      -15

ATG CGG TGG ACT GTG ACA TCA ACT ACG AGG GCC TGG ATM RNN GCN GAA    453
Met Arg Trp Thr Val Thr Ser Thr Thr Arg Ala Trp Ile Xaa Ala Glu
      -10                      -5                      1                      5

CCT CCG CAG CTG GAC ATC TCG                                          474
Pro Pro Gln Leu Asp Ile Ser
                        10
```

(2) INFORMATION FOR SEQ ID NO: 270:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 82..210

(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 49..177
id AA082886
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..83
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 15..51
id AA082886
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 17..97
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq FVLGSARLGGSGS/MR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

AACATTAACC GGCAGG ATG TCG GAG GTG CGG CTG CCA CCG CTA CGC GCC CTG	52
Met Ser Glu Val Arg Leu Pro Pro Leu Arg Ala Leu	
-25 -20	
GAC GAC TTT GTT CTG GGG TCG GCG CGT CTT GGC GGC TCC GGA TCC ATG	100
Asp Asp Phe Val Leu Gly Ser Ala Arg Leu Gly Gly Ser Gly Ser Met	
-15 -10 -5 1	
CGA CCC GCT GCG ATG GTG YHA CCG CGT CAT CAA CAA CCT CCT CTA CTA	148
Arg Pro Ala Ala Met Val Xaa Pro Arg His Gln Gln Pro Pro Leu Leu	
5 10 15	
CCA AAC CAA CTA CCT TCT CTG CTT CGG CAT CGG CCT CGC TCT CGC CGG	196
Pro Asn Gln Leu Pro Ser Leu Leu Arg His Arg Pro Arg Ser Arg Arg	
20 25 30	
GTA CGT ACG GCC ACG	211
Val Arg Thr Ala Thr	
35	

(2) INFORMATION FOR SEQ ID NO: 271:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 177..257
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 107..177
id W93162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..112
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 52..102
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 141..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 132..174
id W67415
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 174..254
id N44655
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 104..174
id N44655

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 41..170
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..240
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..226
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..40
id HSBA7H051
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..183
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 63..169
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 184..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 169..249
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 15..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..39
id R37538
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 206..250
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8

seq LVSATAWLEECWW/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

```
AGGCGGCGGAA GATGGCGGAG AACAGCGGTC GCGCCGGCAA GAGCAGCGGG AGCGNCGCGN    60
GGAAGGGGGC GGTGTCCGCA GAGCAGGTGA TTGCTGGCTT CAACCGCCTT CGGCAGGAAC    120
AGCGAGGCCT GGCATCCAAA GCAGCTGAGT TGGAGATGGA GTTGAATGAG CACAGCCTAG    180
TGAATCGATA CACTGAAGGA GGTAG ATG AAA CTC GTA AGT GCT ACC GCA TGG        232
                Met Lys Leu Val Ser Ala Thr Ala Trp
                -15                               -10

TTG GAG GAR TGC TGG TGG AGC GAA CTG TCA                                262
Leu Glu Glu Cys Trp Trp Ser Glu Leu Ser
-5                               1
```

(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 142..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 120..360
id HUML1108
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 29..139
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 17..127
id HUML1108
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 37..395
id AA156844
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 32..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 137..500
id HSU51712
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 237..395
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 112..270
id T70871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 133..235
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 9..111
id T70871
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 77..185
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 105..213
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 177..286
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 206..315
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 284..317
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 314..347
id H48308
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 309..410
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.3
seq LYPVLLAVCCLES/VV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

```
AAGCTTCCAA ACCCAGGGCT TGCCTTGCC TTTGCCTCTT CCACCGCGCA GGGACCATGT    60
CGGCGGAGAC CGCGAGCGGC CCCACAGAGG ACCAGGTGGA AATCCTGGAG TACAACTTCA   120
ACAAGGTCGA CAAGCACCCG GATTCCACCA CGCTGTGCCT CATCGCGGCC GAGGCAGGCC   180
TTTCCGAGGA GGAGACCCAG AAATGGTTTA AGCAGCGCCT GGCAAAGTGG CGGCGCTCAG   240
AAGGCCTGCC CTCAGAGTGC AGATCCGTCA CAGACTAAGG AGATGGCAGG CATTGACAGC   300
TTCCTCC ATG AAG GCC ATC TCT GTT TCT CTC CTC CGC TTA ACC AAG CTG     350
      Met Lys Ala Ile Ser Val Ser Leu Leu Arg Leu Thr Lys Leu
                -30                      -25

TTG TGG TTT TTC AGC ATA GTG TTG TAT GTT CCA TTG CTA GCT GTC TGC     398
Leu Trp Phe Phe Ser Ile Val Leu Tyr Val Pro Leu Leu Ala Val Cys
-20                -15                      -10                      -5

TGT TTA CAC AGT GTT GTA TTT TTT                                     422
Cys Leu His Ser Val Val Phe Phe
      1
```

(2) INFORMATION FOR SEQ ID NO: 273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..421
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 179..405
id AA010986
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 20..109
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 2..91
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 108..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 91..188
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 443..505
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 429..491
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 417..449
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 402..434
id AA010986
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 1..187
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 316..494
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 300..478
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 195..336
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 95
region 178..319
id W96112
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 69..513
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..445
id W44481
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 2..193
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 195..300
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 184..289
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..405
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 340..396
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 301..352
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 291..342
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 405..448
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 397..440
id AA129812
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..290
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..299
id W40172
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 342..439
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 343..440

id W40172
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 285..342
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 285..342
id W40172
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 85..438
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.8
seq LMIALTVVGCIFM/VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

ACTCCAACGC TGGGTGACAT TGAGCTCACC AGCGCCACCG TCCCCGGCGA AGTTCTGCGC	60
TGGTCGGCGG AGTAGCAAGT GGCC ATG GGG AGC CTC AGC GGT CTG CGC CTG	111
Met Gly Ser Leu Ser Gly Leu Arg Leu	-115 -110
GCA GCA GGA AGC TGT TTT AGG TTA TGT GAA AGA GAT GTT TCC TGN TCT	159
Ala Ala Gly Ser Cys Phe Arg Leu Cys Glu Arg Asp Val Ser Xaa Ser	-105 -100 -95
CTA AGG CTT ACC AGA AGC TCT GAT TTA AAG AGA ATA AAT GGA TTT TGC	207
Leu Arg Leu Thr Arg Ser Ser Asp Leu Lys Arg Ile Asn Gly Phe Cys	-90 -85 -80
ACA AAA CCA CAG GAA AGT CCC GGA GCT CCA TCC CGC ACT TAC AAC AGA	255
Thr Lys Pro Gln Glu Ser Pro Gly Ala Pro Ser Arg Thr Tyr Asn Arg	-75 -70 -65
GTG CCT TTA CAC AAA CCT ACG GAT TGG CAG AAA AAG ATC CTC ATA TGG	303
Val Pro Leu His Lys Pro Thr Asp Trp Gln Lys Lys Ile Leu Ile Trp	-60 -55 -50
TCA GGT CGC TTC AAA AAG GAA ANB NAA ATC CCA GAG ACT GTC TCG TTG	351
Ser Gly Arg Phe Lys Lys Glu Xaa Xaa Ile Pro Glu Thr Val Ser Leu	-45 -40 -35 -30
GAG ATG CTT GAN STT GCA AAG AAC AAG ATG CGA GTG AAG ATC AGC TAT	399
Glu Met Leu Xaa Xaa Ala Lys Asn Lys Met Arg Val Lys Ile Ser Tyr	-25 -20 -15
CTA ATG ATT GCC CTG ACG GTG GTA GGA TGC ATC TTC ATG GTT ATT GAG	447
Leu Met Ile Ala Leu Thr Val Val Gly Cys Ile Phe Met Val Ile Glu	-10 -5 1
GGC AAG AAG GCT GCC CAA AGA CAC GAG ACT TTA ACA AGC TTG MAC TTA	495
Gly Lys Lys Ala Ala Gln Arg His Glu Thr Leu Thr Ser Leu Xaa Leu	5 10 15
GAA AAG AAA GCT CGT CTG	513

Glu Lys Lys Ala Arg Leu
20 25

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..407
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 190..399
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 41..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 35..141
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 91
region 139..198
id AA001815
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..400
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 139..341
id N42162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 60..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 2..147

id N42162
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..354
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 144..300
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 62..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 10..95
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 93..152
id N24414
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..414
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 122..338
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 75..147
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 1..73
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 146..205
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 71..130
id W76137
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 198..360
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 121..283
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 77..147
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 2..72
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 346..402
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 270..326
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 146..205
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 91
region 70..129
id H03817
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 59..358
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq LASSFLFTMGGLG/PI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

ACTGTTTNGG	GGAGGCGCGT	GGGGCTTGAG	GCCGAGAACG	GCCCTTGCTG	CCACCAAC	58
ATG GAG ACT TTG TAC CGT GTC CCG TTC TTA GTG CTC GAA TGT CCC AAC	106					
Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn						
-100 -95 -90 -85						
CTG AAG CTG AAG AAG CCG CCC TGG TTG CAC ATG CCG TCG GCC ATG ACT	154					
Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr						
-80 -75 -70						
GTG TAT GCT CTG GTG GTG GTG TCT TAC TTC CTC ATC ACC GGA GGA ATA	202					
Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile						
-65 -60 -55						
ATT TAT GAT GTT ATT GTT GAA CCT CCA AGT GTC GGT TCT ATG ACT GAT	250					
Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp						
-50 -45 -40						
GAA CAT GGG CAT CAG AGG CCA GTA GCT TTC TTG GCC TAC AGA GTA AAT	298					

Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 -35 -30 -25

GGA CAA TAT ATT ATG GAA GGA CTT GCA TCC AGC TTC CTA TTT ACA ATG 346
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 -20 -15 -10 -5

GGA GGT TTA GGT TTC ATA ATC CTG GAC GGA TCG RNT GCA CCA AAT ATC 394
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Gly Ser Xaa Ala Pro Asn Ile
 1 5 10

CCA AAA CTC AAT AGA TTC 412
 Pro Lys Leu Asn Arg Phe
 15

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 136..238
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
 region 80..182
 id C05215
 est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 73..111
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
 seq MLVLRSGLTALA/SR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CACTCGGGAA GACTTCAGAG AAGTCTCACA AAGGACTCGG CTGGGTGCTT TTCTCAGTGC 60

CGAAGCCGCG CC ATG CTC GTT CTC AGA AGC GGC CTG ACC AAG GCG CTT GCC 111
 Met Leu Val Leu Arg Ser Gly Leu Thr Lys Ala Leu Ala
 -10 -5

TCA CGG ACG CTC GCG CMT CAG AKA AWT TTT GCT CAT CGA GCT GAA GTT 159
 Ser Arg Thr Leu Ala Xaa Gln Xaa Xaa Phe Ala His Arg Ala Glu Val
 1 5 10 15

CGG AAA GCC TTA GCC AAC TGT AAG GAA TGG CAA GAA CAA TCT ATC ATT 207

Arg Lys Ala Leu Ala Asn Cys Lys Glu Trp Gln Glu Gln Ser Ile Ile
20 25 30
CCA AAT TTG GCT CGC ATT GAT AAA CAA GAG ACC AGG 243
Pro Asn Leu Ala Arg Ile Asp Lys Gln Glu Thr Arg
35 40

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 77..206
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 37..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92
region 1..77
id R87832
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 112..241
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 65..194
id HUM427G10B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 49..113
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..65
id HUM427G10B
est

(ix) FEATURE:

- (A) NAME/KEY: other

(B) LOCATION: 112..241
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 52..181
 id R52722
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 62..113
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 92
 region 1..52
 id R52722
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 111..241
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 90
 region 79..209
 id W41484
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 30..137
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq NIESLAWTGGTLG/HP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

GAGTTTCCTG	CGAGCTCGGC	TTCCTCAAC	ATG	GCT	GCG	CCC	TTG	TCA	GTG	GAG	53
	Met	Ala	Ala	Pro	Leu	Ser	Val	Glu			
	-35						-30				
GTG GAG TTC	GGA GGT GGT	GCG GAS	TCC	TGT	TTG	ACG	GTA	TTA	AGA	AAC	101
Val Glu Phe	Gly Gly Ala	Xaa Ser	Cys	Leu	Thr	Val	Leu	Arg	Asn		
	-25		-20				-15				
ATC GAG TCA	CTT GCC TGG	ACA GGA	GGA	ACC	CTG	GGA	CAT	CCG	GAA	CCT	149
Ile Glu Ser	Leu Ala Trp	Thr Gly	Gly	Thr	Leu	Gly	His	Pro	Glu	Pro	
	-10		-5				1				
GCT CAT CTG	GAT CAA GAA	GAA TTT	GCT	AAA	AGA	GCG	GCC	ASA	GTT	GTT	197
Ala His Leu	Asp Gln Glu	Glu Phe	Ala	Lys	Arg	Ala	Ala	Xaa	Val	Val	
	5		10		15				20		
CAT CCA GGG	AGA CAG CGT	GCG GCC	AGG	AAT	TCT	GGT	GCT	GAC	TAC	AGG	245
His Pro Gly	Arg Gln Arg	Ala Ala	Arg	Asn	Ser	Gly	Ala	Asp	Tyr	Arg	
	25		30					35			

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 22..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..382
id AA127626
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 64..349
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 44..329
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 349..403
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 330..384
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 24..60
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 3..39
id W39584
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(47..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 93
region 68..424
id N32838
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: complement(56..403)
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 67..414

id AA121528
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 164..378
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 130..344
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 36..165
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..130
id AA082078
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 198..392
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq FVGGLPVIFWSWA/GL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

```

ACTTAGTCGT GTGTACATCA TTGGGAATGG AGGGAAATAA ATGACTGGAT GGTCGCTGCT   60
TTTAAAGTTT CAAATTGACA TTCCAGACAA GCGGTGCCTG AGCCTGTGCC TGTCTTCAGA  120
TCTTCACAGC ACAGTTCCTG GGAAGGTGGA GCCACCAGCC TCTCCTTGAA TAACTGGGAG  180
ATGAAACAGG AAGCTCT ATG ACA CAC TTG ATC GAA TAT GAC AGA CAC CGA   230
      Met Thr His Leu Ile Glu Tyr Asp Arg His Arg
      -65                               -60                   -55

AAA TCA CGA CTC AGC CCC CTC CAG CAC CTC TAC CTG TTG CCC GCC GAT   278
Lys Ser Arg Leu Ser Pro Leu Gln His Leu Tyr Leu Leu Pro Ala Asp
      -50                               -45                   -40

CAC AGC CGG AAT GCA GCT GAA AGA TTC CCT GGG GCC TGG TTC CAA CCG   326
His Ser Arg Asn Ala Ala Glu Arg Phe Pro Gly Ala Trp Phe Gln Pro
      -35                               -30                   -25

CCC ACT GTG GAC TCT GAG GCC TCT GCA TTT GTG GGT GGT CTG CCT GTG   374
Pro Thr Val Asp Ser Glu Ala Ser Ala Phe Val Gly Gly Leu Pro Val
      -20                               -15                   -10

ATA TTT TGG TCA TGG GCT GGT CTG GTC   401
Ile Phe Trp Ser Trp Ala Gly Leu Val
      -5                               1

```

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Uterus

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 70..337
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 1..268
id HSC2SG081
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 71..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..181
id R13964
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..334
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 184..262
id R13964
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 26..255
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..230
id HUML13589
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 116..251
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 1..136
id H05572
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 256..337
- (C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 100
region 139..220
id H05572
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 24..89
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WARKLLSVPWLLC/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

AACAGTTACG CGCCGCACGG ATC ATG GCC GCA GCC GCT CTG GGG CAG ATC TGG 53
Met Ala Ala Ala Ala Leu Gly Gln Ile Trp
-20 -15

GCA CGA AAG CTT CTC TCT GTC CCT TGG CTT CTG TGT GGT CCC AGA AGA 101
Ala Arg Lys Leu Leu Ser Val Pro Trp Leu Leu Cys Gly Pro Arg Arg
-10 -5 1

TAT GCC TCC TCC AGT TTC AAG GCT GCA GAC CTG CAG CTG GAA ATG ACA 149
Tyr Ala Ser Ser Ser Phe Lys Ala Ala Asp Leu Gln Leu Glu Met Thr
5 10 15 20

CAG AAG CCT CAT AAG AAG CCT GGC CCC GGC GAG CCC CTG GTG TTT GGG 197
Gln Lys Pro His Lys Lys Pro Gly Pro Gly Glu Pro Leu Val Phe Gly
25 30 35

AAG ACA TTT ACC GAC CAC ATG CTG ATG GTG GAA TGG AAT GAC AAG GGC 245
Lys Thr Phe Thr Asp His Met Leu Met Val Glu Trp Asn Asp Lys Gly
40 45 50

TGG GGC CAG CCC CGA ATC CAG CCC TTC CAG AAC CTC ACG CTG CAC CCA 293
Trp Gly Gln Pro Arg Ile Gln Pro Phe Gln Asn Leu Thr Leu His Pro
55 60 65

GCC TCC TCC AGC CTC CAC TAC TCC CTG CAG CTG TTT GAG GGC 335
Ala Ser Ser Ser Leu His Tyr Ser Leu Gln Leu Phe Glu Gly
70 75 80

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 57..176
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 50..169
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 219..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 213..338
id AA126817
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 10..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 2..336
id W79731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..326
id H21245
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 31..302
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 34..305
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 302..344
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 306..348
id H11314
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 41..202
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 22..183
id W19587
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 201..284
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 98
 region 183..266
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 283..344
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 266..327
 id W19587
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 48..161
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.7
 seq CPLLLLVTNNNG/RH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

```

AAGGGGTCGG AGGTCAGGGC GAGCGTCTCG CAGGCCGTAG GAGGAAG ATG GCG GTG      56
                                     Met Ala Val

GAG TCG CGC GTT ACC CAG GAG GAA ATT AAG AAG GAG CCA GAG AAA CCG      104
Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys Glu Pro Glu Lys Pro
-35                               -30                               -25                               -20

ATC GAC CGC GAG AAG ACA TGC CCA CTG TTG CTA CTG GTC TTC ACC ACC      152
Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu Leu Val Phe Thr Thr
                               -15                               -10                               -5

AAT AAC GGC CGC CAC CAC CGA ATG GAC GAG TTC TCC CGG GGA AAT GTA      200
Asn Asn Gly Arg His His Arg Met Asp Glu Phe Ser Arg Gly Asn Val
                               1                               5                               10

CCG TCC AGC GAG TTG CAG ATC TAC ACT TGG ATG GAT GCA ACT TTG AAA      248
Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met Asp Ala Thr Leu Lys
15                               20                               25

GAA CTG ACA AGC TTA GTA AAA GAA GTC TAC CCA GAA GCT AGA WAG AAG      296
Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro Glu Ala Arg Xaa Lys
30                               35                               40                               45

GGC ACT CAC TTC AAT TTT GCA VTC GTT TTT ACA GAT GTT AAA AGA CCT      344
Gly Thr His Phe Asn Phe Ala Xaa Val Phe Thr Asp Val Lys Arg Pro
                               50                               55                               60

```

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 401 base pairs

- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 72..338
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 332..363
id W79829
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 14..280
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 370..401
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 90
region 274..305
id H62624
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 24..290
id H81957
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 111..376
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 92

region 59..324
id W82998
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 111..376
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 64..329
id AA023811
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 240..305
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

ACTAGCCTGC GAGTGTCTCTG AGGGAAGCAA GGAGGCGGCG GCGGCCGCAG CGAGTGGCGA	60
GTAGTGGAAA CGTTGCTTCT GAGGGGTGTC CAAGATGASC GGTTCKAMCG GAGKTCAAGC	120
TGAACCAGCC ACCCGAGGAT GGCATCTCCT CCGTGAAGTT CAGCCCCAAC ACCTCCCACT	180
TCCTGCTTGT CTCCTCCTGG GACACGTCCG TCGTCTCTTA CGATGTGCCG GCCAACTCC	239
ATG CGG CTC AAG TAC CAG CAC ACC GGC GCC GTC CTG GAC TGC GCC TTC	287
Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe	
-20 -15 -10	
TAC GAT CCA ACG CAT GCC TGG AGT GGA GGA CTA GAT CAT CAA TTG AAA	335
Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Gln Leu Lys	
-5 1 5 10	
ATG CAT GAT TTG AAC ACT GAT CAA GAA AAT CTT GTT GGG ACC ATG ATG	383
Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr Met Met	
15 20 25	
CCC CTA TCA GAT GTG TTG	401
Pro Leu Ser Asp Val Leu	
30	

(2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: DOUBLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 72..257
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 47..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 33..75
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 14..47
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..34
id T60345
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 75..260
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 12..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..78
id T46853
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 87..207
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 39..159
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 193..272
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92

region 144..223
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..89
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 1..42
id R57601
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 84..195
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 90
region 55..166
id W71083
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 12..269
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.7
seq WAVVLADTAVTSG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ATAGGCGCAA	G	ATG	GCG	CTG	CTT	TTT	GCA	CGT	TCT	TTG	CGC	TTG	TGC	CGC	50	
	Met	Ala	Leu	Leu	Phe	Ala	Arg	Ser	Leu	Arg	Leu	Cys	Arg			
	-85						-80					-75				
TGG	GGA	GCC	AAA	CGA	TTG	GGA	GTT	GCC	TCC	ACA	GAG	GCC	CAG	AGA	GGC	98
Trp	Gly	Ala	Lys	Arg	Leu	Gly	Val	Ala	Ser	Thr	Glu	Ala	Gln	Arg	Gly	
	-70						-65					-60				
GTC	AGT	TTC	AAA	CTG	GMA	GAA	AAA	ACC	GCC	CAC	AGC	AGC	CTG	GCA	CTC	146
Val	Ser	Phe	Lys	Leu	Xaa	Glu	Lys	Thr	Ala	His	Ser	Ser	Leu	Ala	Leu	
	-55						-50					-45				
TTC	AGA	GAT	GAT	ACG	GGT	GTC	AAA	TAT	GGC	TTG	GTG	GGA	TTG	GAG	CCC	194
Phe	Arg	Asp	Asp	Thr	Gly	Val	Lys	Tyr	Gly	Leu	Val	Gly	Leu	Glu	Pro	
	-40						-35					-30				
ACC	AAG	GTG	GCC	TTG	AAT	GTG	GAG	CGC	TTC	CGG	GAG	TGG	GCA	GTG	GTG	242
Thr	Lys	Val	Ala	Leu	Asn	Val	Glu	Arg	Phe	Arg	Glu	Trp	Ala	Val	Val	
	-25					-20				-15				-10		
CTG	GCA	GAC	ACA	GCG	GTC	ACC	AGT	GGC	AGA	GGG						275
Leu	Ala	Asp	Thr	Ala	Val	Thr	Ser	Gly	Arg	Gly						
				-5						1						

(2) INFORMATION FOR SEQ ID NO: 282:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE.
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 77..280
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.6
seq ILLGNYCVAVADA/KK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```

ATTCCCCCTT GGGCGGTGGT GGAGGTGGTA ACCGTGATAG TAGCAGCTCC GGCGGCAGCA    60
ACAGCGACTA CGAGGG ATG GCG GCG GCT GCA GCA GGA ACT SNA ACA TCC CAG    112
          Met Ala Ala Ala Ala Ala Gly Thr Xaa Thr Ser Gln
                   -65                               -60

AGG TTT TTC CAG AGC TTC TCG GAT GCC CTA ATC GAC GAG GAC CCC CAG    160
Arg Phe Phe Gln Ser Phe Ser Asp Ala Leu Ile Asp Glu Asp Pro Gln
   -55                               -50                               -45

GCG GCG TTA GAG GAG CTG ACT AAG GCT TTG GAA CAG AAA CCA GAT GAT    208
Ala Ala Leu Glu Glu Leu Thr Lys Ala Leu Glu Gln Lys Pro Asp Asp
   -40                               -35                               -30                               -25

GCA CAG TAT TAT TGT CAA AGA GCT TAT TGT CAC ATT CTT CTT GGG AAT    256
Ala Gln Tyr Tyr Cys Gln Arg Ala Tyr Cys His Ile Leu Leu Gly Asn
          -20                               -15                               -10

TAC TGT GTT GCT GTT GCT GAT GCA AAG AAG TCT CTA GAA CTC AAT CCA    304
Tyr Cys Val Ala Val Ala Asp Ala Lys Lys Ser Leu Glu Leu Asn Pro
          -5                               1                               5

AAT AAT TCC ACT GCT ATG CTG AGA AAA GGA ATA TGT GAA TAC CAT GAA    352
Asn Asn Ser Thr Ala Met Leu Arg Lys Gly Ile Cys Glu Tyr His Glu
      10                               15                               20

AAA AAC TAT GCT GCT GCC CTA GAA ACT TTT TAC AGA AGG ACG GGG    397
Lys Asn Tyr Ala Ala Ala Leu Glu Thr Phe Tyr Arg Arg Thr Gly
      25                               30                               35

```

(2) INFORMATION FOR SEQ ID NO: 283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 78..379
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 79..380
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 4..55
id H17763
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 96..377
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 82..363
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 2..53
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 7..58
id H16532
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 79..370
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 46..337
id R52491
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 66..248
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 65..247
id R21494
est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 2..53
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 100
 region 1..52
 id R21494
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 266..305
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 97
 region 268..307
 id R21494
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 129..321
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 71..263
 id AA084554
 est

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 315..379
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 96
 region 256..320
 id AA084554
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 139..318
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq WFYIGSSLNGTRG/KR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```

AGTGGCCCGG ATGTTCCGGTG CAGCTGCCAG ATCCGCTGAT CTAGTGCTTC TCGAAAAAAA   60
CCTTCAGGCG GCCCATGGCT GTCGATATTC AACCAGCATG CCTTGGACTT TATTSYGGGA   120
AGACCCTATT ATTTAAAA ATG GCT CAA CTG AAA TAT ATG GAG AAT GTG GGG   171
          Met Ala Gln Leu Lys Tyr Met Glu Asn Val Gly
          -60                               -55                               -50
TAT GCC CAA GAG GAC AGA GAA CGA ATG CAC AGA AAT ATT GTC AGC CTT   219
Tyr Ala Gln Glu Asp Arg Glu Arg Met His Arg Asn Ile Val Ser Leu
          -45                               -40                               -35
GCA CAG AAT CTC CTG AAC TTT ATG ATT GGC TCT ATC TTG GAT TTA TGG   267
Ala Gln Asn Leu Leu Asn Phe Met Ile Gly Ser Ile Leu Asp Leu Trp
          -30                               -25                               -20

```

CAA TGC TTC CTC TGG TTT TAC ATT GGT TCT TCA TTG AAT GGT ACT CGG	315
Gln Cys Phe Leu Trp Phe Tyr Ile Gly Ser Ser Leu Asn Gly Thr Arg	
-15 -10 -5	
GGA AAA AGA GTT CCA GCG CAC TTT TCC AAC ACA TCA CTG CAT TAT TTG	363
Gly Lys Arg Val Pro Ala His Phe Ser Asn Thr Ser Leu His Tyr Leu	
1 5 10 15	
AAT GCA GCA TGG CCG CGG	381
Asn Ala Ala Trp Pro Arg	
20	

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 3..294
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..292
id HUM524F05B
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 44..172
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 48..176
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 167..276
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 170..279
id H81799
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 14..43
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97

region 16..50
id H81799
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 48..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 57..181
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..226
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 93
region 175..234
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 1..45
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 7..51
id T84779
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..294
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 101..228
id W81213
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 66..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..107
id W81213
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 8..172
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..165
id AA090080
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 167..210

(C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 93
 region 159..202
 id AA090080
 est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: 174..266
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.5
 seq WSPLSTRSGGTHA/CS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```

AAAAACAATA GGACGGAAAC GCCGAGGAAC CCGGCTGAGG CGGCAGAGCA TCCTGGCCAG   60
AACAAGCCAA GGAGCCAAGA CGAGAGGGAC ACACGGACAA ACAACAGACA GAAGACGTAC  120
TGGCCGCTGG ACTCCKCTGC CTCCCCATC TCCCGCCAT CTGCGCCCGG AGG ATG      176
                                     Met
AGC CCA GCC TTC AGG GCC ATG GAT GTG GAG CCC CGC GCC AAA GGS TCC      224
Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly Ser
-30                               -25                -20                -15

TTC TGG AGC CCT TTG TCC ACC AGG TCG GGG GGC ACT CAT GCG TGC TCC      272
Phe Trp Ser Pro Leu Ser Thr Arg Ser Gly Gly Thr His Ala Cys Ser
          -10                               -5                        1

GCT TCA ATG AGA CAA CCC TGG                                          293
Ala Ser Met Arg Gln Pro Trp
          5
  
```

(2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 347 base pairs
 (B) TYPE: NUCLEIC ACID
 (C) STRANDEDNESS: DOUBLE
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: other
 (B) LOCATION: 26..326
 (C) IDENTIFICATION METHOD: blastn
 (D) OTHER INFORMATION: identity 99
 region 42..342
 id R71425
 est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 19..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 11..337
id AA133412
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..345)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 172..403
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(71..114)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 402..445
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(26..76)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 439..489
id AA156940
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 172..345
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 186..359
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 72..171
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 83..182
id W07240
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..76
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 92
region 33..88
id W07240
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 39..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..307
id R81019
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 18..179
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq SILAQVLDQSARA/RL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```

AGCGCTGACG CCGAGCC ATG GCG GAC GAG GAG CTT GAG GCG CTG AGG AGA      50
      Met Ala Asp Glu Leu Leu Glu Ala Leu Arg Arg
                        -50                      -45

CAG AGG CTG GCC GAG CTG CAG GCC AAA CAC GGG GAT CCT GGT GAT GCG      98
Gln Arg Leu Ala Glu Leu Gln Ala Lys His Gly Asp Pro Gly Asp Ala
      -40                      -35                      -30

GCC CAA CAG GAA GCA AAG CAC AGG GAA GCA GAA ATG AGA AAC AGT ATC      146
Ala Gln Gln Glu Ala Lys His Arg Glu Ala Glu Met Arg Asn Ser Ile
      -25                      -20                      -15

TTA GCC CAA GTT CTG GAT CAG TCG GCC CGG GCC AGG TTA AGT AAC TTA      194
Leu Ala Gln Val Leu Asp Gln Ser Ala Arg Ala Arg Leu Ser Asn Leu
      -10                      -5                      1                      5

GCA CTT GTA AAG CCT GAA AAA ACT AAA GCA GTA GAG AAT TAC CTT ATA      242
Ala Leu Val Lys Pro Glu Lys Thr Lys Ala Val Glu Asn Tyr Leu Ile
      10                      15                      20

CAG ATG GCA AGA TAT GGA CAA CTA AGT GAG AAG GTA TCA GAA CAA GGT      290
Gln Met Ala Arg Tyr Gly Gln Leu Ser Glu Lys Val Ser Glu Gln Gly
      25                      30                      35

TTA ATA GAR ATC CTT AAA AAA GTA AGC CAA CAA ACA GAA AAG AHN ACA      338
Leu Ile Glu Ile Leu Lys Lys Val Ser Gln Gln Thr Glu Lys Xaa Thr
      40                      45                      50

ACA GTG AGG
Thr Val Arg
      55

```

347

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 186..382

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 156..352
id AA082259
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 61..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 34..119
id AA082259
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 29..61

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 96
region 1..33
id AA082259
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 194..331

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 97
region 169..306
id H80945
est

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 54..146

(C) IDENTIFICATION METHOD: blastn

(D) OTHER INFORMATION: identity 93
region 30..122
id H80945
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 157..345

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 3.5
seq GLVCAGLADMARPAE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AACAGCGGGC AGGGAAAGCC GCGGGAAGGG TACTCCAGGC GAGAGGCGGA CGCGAGTCGT      60
CGTGGCAGGA AAAGTGACTA GCTCCCCTTC GTTGTGAGCC AGGGACGAGA ACACAGCCAC      120
GCTCCCAMCC GGCTGCCHAA GRWTCCTTSG GCGGCG ATG TCG GCC GCC GGT GCC      174
                               Met Ser Ala Ala Gly Ala
                               -60
CGA GGC CTG CGG GCC ACC TAC CAC CGG CTC CTC GAT AAA GTG GAG CTG      222
Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
-55                               -50                               -45
ATG CTG CCC GAG AAA TTG AGG CCG TTG TAC AAC CAT CCA GCA GGT CCC      270
Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
-40                               -35                               -30
AGA ACA GTT TTC TTC TGG GCT CCA ATT ATG AAA TGG GGG TTG GTG TGT      318
Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
-25                               -20                               -15                               -10
GCT GGA TTG GCT GAT ATG GCC AGA CCT GCA GAA AAA CTT AGC ACA GCT      366
Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
-5                               1                               5
CAA TCT GVK GTT TTG ATG GCT ACA GGG TTT ATT TGG TCA AGA TAC TCG      414
Gln Ser Xaa Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser
10                               15                               20

```

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 196..391
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 95
region 185..380
id W07314
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 58..204
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 46..192
id W07314

est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 409..478
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 401..470
id W07314
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 34..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 12..390
id W07582
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 45..393
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 31..379
id W73850
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 16..52
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 1..37
id W73850
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 73..447
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..375
id AA112776
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 63..388
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..326
id H72671
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 98..355
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5

seq TGXLNMTLORASA/AP

(xi) SEQUENCE DESCRIPTION: SEQ.ID NO: 287:

AACTTGTCAG	CCCTTGCTCTG	AGGCGGAGGC	AGCCCCGCGC	CGCGCCGGAC	CCGAGCATAT	60
TTCATTTTCT	GTCATTGGAC	TTTGAGCCAT	TAGAACC	ATG AGC AAC TAC AGT GTG	115	
				Met Ser Asn Tyr Ser Val		
				-85		
TCA CTG GTT GGC CCA GCT CCT TGG GGT TTC CGG CTG CAG GGC GGT AAG	163					
Ser Leu Val Gly Pro Ala Pro Trp Gly Phe Arg Leu Gln Gly Gly Lys						
-80 -75 -70 -65						
GAT TTC AAC ATG CCT CTG ACA ATC TCT AGT CTA AAA GAT GGC GGC AAG	211					
Asp Phe Asn Met Pro Leu Thr Ile Ser Ser Leu Lys Asp Gly Gly Lys						
-60 -55 -50						
GCA GCC CAG GCA AAT GTA AGA ATA GGC GAT GTG GTT CTC AGC ATT GAT	259					
Ala Ala Gln Ala Asn Val Arg Ile Gly Asp Val Val Leu Ser Ile Asp						
-45 -40 -35						
GGA ATA AAT GCA CAA GGA ATG ACT CAT CTT GAA GCC CAG AAT AAG ATT	307					
Gly Ile Asn Ala Gln Gly Met Thr His Leu Glu Ala Gln Asn Lys Ile						
-30 -25 -20						
AAG GGT TGT ACA GGA NYT TTG AAT ATG ACT CTG CAA AGA GCA TCT GCT	355					
Lys Gly Cys Thr Gly Xaa Leu Asn Met Thr Leu Gln Arg Ala Ser Ala						
-15 -10 -5						
GCA CCC AAG CCT GAG CCG GTT CCT GTT CAA AAG CCC ACA GTC ACC AGC	403					
Ala Pro Lys Pro Glu Pro Val Pro Val Gln Lys Pro Thr Val Thr Ser						
1 5 10 15						
GTG TGT TCC GAG ACT TCT CAG GAG CTA GCA GAG GGA CAG AGA AGA GGA	451					
Val Cys Ser Glu Thr Ser Gln Glu Leu Ala Glu Gly Gln Arg Arg Gly						
20 25 30						
TCC CAG GGT GAC AGT AAA CAG CAA AAT	478					
Ser Gln Gly Asp Ser Lys Gln Gln Asn						
35 40						

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(11) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

(F) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Uterus

(ix) FEATURE:

(A) NAME/KEY: other

(B) LOCATION: 4..333
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..330
id N35568
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 26..297
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 1..272
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 295..338
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 271..314
id R35915
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 44..255
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 1..212
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 251..355
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 98
region 209..313
id W31312
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 21..328
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 99
region 13..320
id HSC1MA011
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 62..339
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 97
region 1..278
id R61491
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 245..298
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq LLGLELSEAEAIG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

```
ATTCGTTTAC AGTTCGGCAC GTAGGACGGA GGGTAGTGCG TCTAGAGACA CATATTCCCA    60
ACGGATTGTA CGATGGTGTT CGGTCTTGAA TGGAAATGTA GTCTTAGGCC AGTCTTAGGT   120
TTTTGAACAG GATAGTAGGT ATCCGGAGTC GATTGAGGGC CAGAGCAGGC ACTGGGGTTC   180
GGATCCTGGG CAAAGTTTCC CACATTGAGG GTCTCGAGGA CGCCTAGATC TCTTTCCCAG   240
GGCC ATG GCG AAC CCG AAG CTG CTG GGA CTG GAG CTA AGC GAG GCG GAG   289
Met Ala Asn Pro Lys Leu Leu Gly Leu Glu Leu Ser Glu Ala Glu
      -15                      -10                      -5

GCG ATC GGT GCT GAT TCG GCG CGA TTT GAG GAG CTG CTG CTG CAG GCC   337
Ala Ile Gly Ala Asp Ser Ala Arg Phe Glu Glu Leu Leu Leu Gln Ala
      1                      5                      10

TCG AAG GAG CTC CAG CAA
Ser Lys Glu Leu Gln Gln
      15
```

(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 113..201
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 90..178
id W21193
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 23..74
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98

region 2..53
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: 71..111
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 100
region 49..89
id W21198
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061731
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(114..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 94
region 271..358
id AA061768
est

(ix) FEATURE:

(A) NAME/KEY: other
(B) LOCATION: complement(125..201)
(C) IDENTIFICATION METHOD: blastn
(D) OTHER INFORMATION: identity 96
region 269..345
id AA058174
est

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 204..323
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq ALLCTLLLLHFQNI/RR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

```
AAAGGTGTCT GGATCGGAGG GAGGTTCTGGG TGGGCATCGG GCGGCTGGAA GAGCTCGACT    60
CGTCCCGCTG GGAAAGCGCG AGTCTGAGTG GAACCCTGGA CGACTTGCAG AGCGGCTGGC    120
GCACTCATGG CGGACTACTG GAAGTCACAG CCAAAGAAAT TCTGTGATTA CTGCAAGTGC    180
TGGATAGCAG ACAATAGGCC TGT ATG ATA ATT CCG CTG TTA GAG ATT CTA ATA    233
                Met Ile Ile Pro Leu Leu Glu Ile Leu Ile
                -40                                -35
ATA ATT TTG TTG AAT GAA GTG CTC CTT TTT GAT GTA AAC TCA GTT TAC    281
```

Ile Ile Val Leu Asn Glu Val Leu Leu Phe Asp Val Asn Ser Val Tyr	
-30 -25 -20 -15	
AAA GCA CTT TTA TGT ACA TTG CTC TTG CAT TTT CAA AAC ATC AGA AGA	329
Lys Ala Leu Leu Cys Thr Leu Leu Leu His Phe Gln Asn Ile Arg Arg	
-10 -5 1	
TTT CTG TCT TCT CAG TCC CCT ATG AAA GCT GTG AGC CTT CTA THT TTT	377
Phe Leu Ser Ser Gln Ser Pro Met Lys Ala Val Ser Leu Leu Xaa Phe	
5 10 15	
CAT CAA CCT GAC TTT GAT TAT ATA	401
His Gln Pro Asp Phe Asp Tyr Ile	
20 25	

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..382
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 97
region 4..337
id HUMGPCRB
vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 292..345
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 1..54
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 345..382
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 94
region 55..92
id T29782
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 80..235

(C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 7.4
 seq LVFIIGLVGNLLA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

```

AACTTCAGTT TGGACAACTA CTCACAGCTA CTACACAGAG ACCCGAACGA GTCAGTGATA    60
TACACCTGGA CCACCACCA ATG GAT ATA CAA ATG GCA AAC AAT TTT ACT CCG    112
          Met Asp Ile Gln Met Ala Asn Asn Phe Thr Pro
          -50                               -45

CCC TCT GCA ACT CCT CAG GGA AAT GAC TGT GAC CTC TAT GCA CAT CAC    160
Pro Ser Ala Thr Pro Gln Gly Asn Asp Cys Asp Leu Tyr Ala His His
-40                               -35                               -30

AGC ACG GCC AGG ATA GTA ATG CCT CTG CAT TAC AGC CTC GTC TTC ATC    208
Ser Thr Ala Arg Ile Val Met Pro Leu His Tyr Ser Leu Val Phe Ile
-25                               -20                               -15                               -10

ATT GGG CTC GTG GGA AAC TTA CTA GCC TTG GTC GTC ATT GTT CAA AAC    256
Ile Gly Leu Val Gly Asn Leu Leu Ala Leu Val Val Ile Val Gln Asn
          -5                               1                               5

AGG AAA AAA ATC AAC TCT ACC ACC CTC TAT TCA ACA AAT TTG GTT ATT    304
Arg Lys Lys Ile Asn Ser Thr Thr Leu Tyr Ser Thr Asn Leu Val Ile
          10                               15                               20

TCT GAT ATA CTT TTT ACC ACC GCT TTG CCT ACA CGA ATA GCT ACT ATG    352
Ser Asp Ile Leu Phe Thr Thr Ala Leu Pro Thr Arg Ile Ala Thr Met
          25                               30                               35

CMA TGG GCY TTG ACT GGA GAA TCG GAG ATG TGG    385
Xaa Trp Ala Leu Thr Gly Glu Ser Glu Met Trp
          40                               45                               50
  
```

(2) INFORMATION FOR SEQ ID NO: 291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: DOUBLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: CDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Pancreas

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..462
- (C) IDENTIFICATION METHOD: fasta
- (D) OTHER INFORMATION: identity 99
 region 1..408
 id HUMORF06
 vrt

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 47..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..218
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..412
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 216..365
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 412..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 366..416
id W77946
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..409
id C16991
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 212..411
id N28784
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 97
region 52..214
id N28784
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 50..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..58

id N28784
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 54..356
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 99
region 1..303
id C17735
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 357..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 303..408
id C17735
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 102..264
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 96
region 47..209
id AA057588
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 263..406
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 98
region 207..350
id AA057588
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 406..462
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 351..407
id AA057588
est

(ix) FEATURE:

- (A) NAME/KEY: other
- (B) LOCATION: 55..107
- (C) IDENTIFICATION METHOD: blastn
- (D) OTHER INFORMATION: identity 100
region 1..53
id AA057588
est

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 357..443 -
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7
seq SMIGIGSLPSCWA/CW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

```

AGTTCGTTTA TTCCTCCGCG CGCTGGGACA GGCTGCTTCT TCGCCAGAAC CAACCGGTTG   60
CTTGCTGTCC CAGCGGCGCC CCCTCATCAC CGTCGCCATG CCCGGAGGTC TGCTTCTCGG   120
GGACGTGGCT CCCAACTTTG AGGCCAATAC CACCGTCGGC CGCATCCGTT TCCACGACTT   180
TCTGGGAKAC TCATGGGGCA TTCTCTTCTC CCACCCTCGG GACTTTACCC CASTGTGCAC   240
CACAGAGCTT GGCAGAGCTG CAAAGCTGGC ACCAGAATTT GCCAAGAGGA ATGTTAAGTT   300
GWTTGCCCTT TCAATAGACA GTGTTGAGGA CCATCTTGCC TGGAGCAAGG ATATCA ATG   359
                                   Met
CTT ACA ATT GTG AAG AGC CCA CAG AAA AGT TAC CTT TTC CCA TCA TCG   407
Leu Thr Ile Val Lys Ser Pro Gln Lys Ser Tyr Leu Phe Pro Ser Ser
               -25                      -20                      -15

ATG ATA GGA ATC GGG AGC TTG CCA TCC TGT TGG GCA TGC TGG ATC CAG   455
Met Ile Gly Ile Gly Ser Leu Pro Ser Cys Trp Ala Cys Trp Ile Gln
               -10                      -5                      1

CAG AGA
Gln Arg
  5
                                   461

```

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Liver

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -35..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 15
seq LFLLLLLLAASAWG/VT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

```

Met Ser Ser Trp Ser Arg Gln Arg Pro Lys Ser Pro Gly Gly Ile Gln
-35                      -30                      -25                      -20

Pro His Val Ser Arg Thr Leu Phe Leu Leu Leu Leu Ala Ala Ser
      -15                      -10                      -5

```

Ala Trp Gly Val Thr Leu Ser Pro Lys Asp Cys Gln Val Phe Arg Ser
 1 5 10
 Asp His Gly Ser Ser Ile Ser Cys Gln Pro Pro Ala Glu Ile Pro Gly
 15 20 25
 Tyr Leu Pro Ala Thr
 30

(2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.2
seq LLLXAVLLSLASA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Xaa Ala Val Leu Leu
 -20 -15 -10
 Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp Glu Ser
 -5 1 5 10
 Leu Asp Ser Lys Thr Thr Leu Thr Ser Asp Glu Ser Val Lys Asp His
 15 20 25
 Thr Thr Ala Gly Arg Val Val Ala Gly Gln Ile Phe Leu Asp Ser Glu
 30 35 40
 Glu Ser Glu Leu Glu Xaa Ser Ile Gln Glu Glu Glu Asp Ser Leu Lys
 45 50 55
 Ser Gln Glu Gly Glu Ser Val Thr Glu Asp Ile Ser Phe Leu Glu Ser
 60 65 70 75

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 13.1
seq CVLLLLLLLLLTRS/SE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu
-20 -15 -10
Leu Leu Thr Arg Ser Ser Glu Val Glu Xaa Xaa Ala Glu Val Gly Gln
-5 1 5 10
Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
15 20 25
Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
30 35 40
Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
45 50 55
Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr
60 65 70 75
Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
80 85 90
Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu
95 100

(2) INFORMATION FOR SEQ ID NO: 295:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -21..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.6
seq LLFLFLAVDEAWA/GM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

Met Gly Pro Val Arg Leu Gly Ile Leu Leu Phe Leu Phe Leu Ala Val
-20 -15 -10

Asp Glu Ala Trp Ala Gly Met Leu Lys Glu Glu Gly Arg
-5 1 5

(2) INFORMATION FOR SEQ ID NO: 296: -

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.7
seq SLLLAVALGLATA/VS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

Met Lys Ser Leu Ser Leu Leu Leu Ala Val Ala Leu Gly Leu Ala Thr
-15 -10 -5

Ala Val Ser Ala Gly Pro Ala Val Ile Glu Cys Trp Phe Val Glu Asp
1 5 10 15

Ala Ser Gly Lys Gly Leu Ala Lys Arg Pro Gly Ala Leu Leu Leu Arg
20 25 30

Gln Gly Pro Gly Glu Pro Pro Pro Arg Pro Asp Leu Asp Pro Glu Leu
35 40 45

Tyr Leu Ser Val His Asp Pro Ala Gly Ala Leu Gln Ala Arg
50 55 60

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -16..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.6
seq LLTLXLLGGPTWA/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

Met Leu Leu Leu Leu Thr Leu Xaa Leu Leu Gly Gly Pro Thr Trp Ala
-15 -10 -5
Gly Lys Met Tyr Gly Pro Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu
1 5 10 15
Asp Tyr Asp His Glu Ile Thr Gly Leu Arg Val Ser Val Gly Leu Leu
20 25 30
Leu Val Lys Ser Val Gln Val Lys Leu Gly Asp Ser Trp Asp Val Lys
35 40 45
Leu Gly Ala Leu Xaa Gly Asn Thr Gln Glu Val Xaa Xaa Gln Pro Gly
50 55 60
Glu Tyr Ile Thr Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly
65 70 75 80
Met Val Met Tyr Thr Ser Lys Asp Arg
85

(2) INFORMATION FOR SEQ ID NO: 298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -46..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.4
seq LIILIXIWIWCLG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

```

Met Lys Ile Gly Ile Leu Leu Ser Leu Leu Asn Ser Val Ile Ser Gln
-45                               -40                               -35

Thr Leu Met Ser Cys Asn Trp Lys Gln Gln Met Arg Arg Met Lys Thr
-30                               -25                               -20                               -15

Ile Leu Ile Ile Leu Ile Xaa Ile Trp Ile Trp Cys Leu Gly Ser Gln
                               -10                               -5                               1

Thr Phe Gly Thr Ser Thr Thr Lys Ser Val Gln Leu Lys Ile Leu Arg
      5                               10                               15

Gln Asn Leu Ser His Phe Leu Gln Pro Pro Gln Val Ile
20                               25                               30

```

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.4
seq LPFLLSLFPGALP/VQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

```

Met Lys Ala Ser Ser Gly Arg Cys Gly Leu Val Arg Trp Leu Gln Val
-30                               -25                               -20                               -15

Leu Leu Pro Phe Leu Leu Ser Leu Phe Pro Gly Ala Leu Pro Val Gln
                               -10                               -5                               1

Ile Arg Tyr Ser Ile Pro Glu Glu Leu Ala Lys Asn Ser Val Val Gly
      5                               10                               15

Asn Leu Ala Lys Asp Leu Gly Leu Ser Val Arg Asp Leu Pro Ala Arg
20                               25                               30

Lys Leu Arg Val Ser Ala Glu Lys Glu Tyr Phe Thr Val Asn Pro Glu
35                               40                               45                               50

Ser Gly Asp Leu Leu Val Ser Asp Arg Ile Asp Arg Asp Val
                               55                               60

```

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -33..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq IIFLCHLLRGLHA/XT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

Met Ile Val Asp Cys Val Ser Ser His Leu Lys Lys Thr Gly Asp Gly
-30 -25 -20

Ala Lys Thr Phe Ile Ile Phe Leu Cys His Leu Leu Arg Gly Leu His
-15 -10 -5

Ala Xaa Thr Asp Arg Glu Lys Asp Pro Leu Met Cys Glu Asn Ile Gln
1 5 10 15

Thr His Gly Arg Leu Pro
20

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -104..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.1
seq LTSLSWLLXASCS/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

Met Ala Lys Ala Leu Leu Phe Pro Ser Gly Arg Ser Val Arg Val Leu

```

-100          -95          -90
Tyr Gly Ala Val Asn Lys Glu Arg Gln Xaa Glu Ser Val Leu Asn Arg
-85          -80          -75
Ala Cys Pro Pro Lys Ala Asn Ser Lys Glu Arg Arg Gly Arg Ala Val
-70          -65          -60
Leu Gly Ala Glu Leu Thr Gln Trp Ser Ser Pro Thr Thr Ala Gly Ser
-55          -50          -45
Cys Cys Ser Ser Cys Thr Leu Cys Ala Arg Ser Ser Ser Xaa Val Ile
-40          -35          -30          -25
Ala Pro Ser Pro Leu Val Pro Phe Thr Ser Gly Leu Thr Ser Leu Ser
-20          -15          -10
Trp Leu Leu Xaa Ala Ser Cys Ser Lys Pro Xaa Lys Gly
-5          1          5

```

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -73..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8
seq LATKLLSLSGVFA/VH

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

```

Met Ala Ala Ser Glu Ala Ala Val Val Ser Ser Pro Ser Leu Lys Thr
-70          -65          -60
Asp Thr Ser Pro Val Leu Glu Thr Ala Gly Thr Val Ala Ala Met Ala
-55          -50          -45
Ala Thr Pro Ser Ala Arg Ala Ala Ala Ala Val Val Ala Ala Ala Ala
-40          -35          -30
Arg Thr Gly Ser Glu Ala Arg Val Ser Lys Ala Ala Leu Ala Thr Lys
-25          -20          -15          -10
Leu Leu Ser Leu Ser Gly Val Phe Ala Val His Lys Pro Lys Gly Pro
-5          1          5
Thr Ser Ala Glu Leu Leu Asn Arg Leu Lys Glu Lys Leu Leu Ala Glu

```

10 15 20
 Ala Gly Met Pro Ser Pro Glu Trp Thr Xaa Arg Lys Lys Gln Thr Xaa
 25 30 35
 Glu Asn Trp Ala Trp Arg Asp Ser Arg Gln Arg Xaa Arg Gly Val Leu
 40 45 50 55
 Val Val Gly Ile Gly Ala
 60

(2) INFORMATION FOR SEQ ID NO: 303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8
seq VLWLISFFTFDGD/HG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

Met Lys Val Gly Val Leu Trp Leu Ile Ser Phe Phe Thr Phe Thr Asp
 -15 -10 -5
 Gly His Gly Gly Phe Leu Gly Val Ser Trp Cys Tyr Val Ser Tyr Leu
 1 5 10 15
 Phe Ser Thr Asn Ser Pro Leu Ser Phe Arg Arg Met
 20 25

(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Surrenals

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq WIFLAAILKGVQC/EV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

```

Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
      -15                      -10                      -5

Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
      1                      5                      10

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe
      15                      20                      25

Thr Asp Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
      30                      35                      40                      45

Glu Trp Val Ala Asn Ile Xaa Ser Thr Ala Ser Gly Gly Thr Arg Gly
      50                      55                      60

Tyr Ala Ala Pro Val Lys Asp Arg Phe Ile Ile Ser Arg Asp Asp Ser
      65                      70                      75

Arg Asn Thr Leu His Leu Gln Met Asn Gly Leu Lys Xaa Met Thr Gln
      80                      85                      90

Ala Ile Tyr Tyr Cys Ala Thr
      95                      100

```

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -37..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4
seq LWRLLLWAGTAFQ/VX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

```

Met Ala Glu Pro Gly His Ser His His Leu Ser Ala Arg Val Arg Gly
      -35                      -30                      -25

```

```

Arg Thr Glu Arg Arg Ile Pro Arg Leu Trp Arg Leu Leu Leu Trp Ala
-20          -15          -10
Gly Thr Ala Phe Gln Val Xaa Gln Gly Xaa Xaa Pro Glu Leu Xaa Ala
-5          1          5          10
Cys Lys Glu Ser Glu Tyr His Tyr Glu Tyr Thr Ala Cys Asp Ser Thr
15          20          25
Gly Ser Arg Trp Arg Val Ala Val Pro His Thr Xaa Gly Leu Cys Thr
30          35          40
Ser Leu Pro Asp Pro Val Lys Gly Thr Glu Cys Xaa Xaa Ser Cys Asn
45          50          55
Ala Gly Glu Phe Leu Asp Met Lys Asp Gln Ser Cys Xaa Pro Cys Ala
60          65          70          75
Glu Gly Arg Tyr Ser Leu Gly Thr Gly Ile Arg Phe Asp Glu Trp Asp
80          85          90
Glu Leu Pro His Gly Phe Ala Ala Ser Gln Pro Thr Trp Ser Trp Met
95          100          105
Thr Val Leu Leu Ser His
110

```

(2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq QACLLGLFALILS/GK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

```

Met Thr Ala Asp Pro Arg Lys Gly Arg Met Gly Leu Gln Ala Cys Leu
-25          -20          -15          -10
Leu Gly Leu Phe Ala Leu Ile Leu Ser Gly Lys Cys Ser Xaa Ser Pro
-5          1          5
Glu Pro Asp Gln Arg Arg Thr Leu Pro Pro Gly Trp Val Ser Leu Gly
10          15          20

```



```

Arg Ala Asp Pro Glu Glu Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln
 25                      30                      35

Gln Asn Val Glu Arg Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro
 40                      45                      50                      55

Ser Ser Pro Gln Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp
                      60                      65                      70

Leu Val Arg Pro Ser Pro Leu Thr Pro
 75                      80

```

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LCFLLLAVAMSFF/GS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

```

Met Leu Val Asp Gly Pro Ser Glu Arg Pro Ala Leu Cys Phe Leu Leu
-20                      -15                      -10

Leu Ala Val Ala Met Ser Phe Phe Gly Ser Ala Leu Ser Ile Asp Glu
-5                      1                      5

Thr Arg Ala His Leu Leu Leu Lys Xaa Lys Met Met Arg Leu Gly Gly
10                      15                      20

Arg Leu Val Leu Asn Thr Lys Glu Glu Leu Ala Asn Glu Arg Leu Met
25                      30                      35                      40

Thr Leu Xaa Ile Ala Glu Met Lys Glu Ala Met Arg Thr Leu Ile Phe
45                      50                      55

Pro Pro Ser Met His Phe Phe
60

```

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -17..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.8
seq LVLVLVVAVTVRA/AL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

Met Ala Ala Pro Leu Val Leu Val Leu Val Val Ala Val Thr Val Arg
-15 -10 -5
Ala Ala Leu Phe Arg Ser Ser Leu Ala Glu Phe Ile Ser Glu Arg Val
1 5 10 15
Glu Val Val Ser Pro Leu Ser Ser Trp Lys Arg Val Val Glu Gly Leu
20 25 30
Ser Leu Leu Asp Leu Gly Val Ser Pro Tyr Ser Gly Ala Val Phe His
35 40 45
Glu Thr Pro Leu Ile Ile Tyr Leu Phe His Phe Leu Ile Asp Tyr Ala
50 55 60
Glu Leu Val Phe Met Ile Thr Asp Ala Leu Thr Ala Ile Ala Leu Tyr
65 70 75
Phe Ala Ile Gln Asp Phe Asn Lys Val Val Phe Lys Lys Gln Lys Leu
80 85 90 95
Leu Leu Glu Leu Asp Gln Tyr Ala Pro Asp Val Ala Glu Leu Ile Arg
100 105 110

(2) INFORMATION FOR SEQ ID NO: 309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -102..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.7
 seq LXMTLMPLPKILS/DS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

```

Met Thr Ala Ala Ile Arg Arg Gln Arg Glu Leu Ser Ile Leu Pro Lys
   -100                      -95                      -90

Val Thr Leu Glu Ala Met Asn Thr Thr Val Met Gln Gly Phe Asn Arg
   -85                      -80                      -75

Ser Glu Arg Cys Pro Arg Asp Thr Arg Ile Val Gln Leu Val Phe Pro
   -70                      -65                      -60                      -55

Ala Leu Tyr Thr Val Val Phe Leu Thr Gly Ile Leu Leu Asn Thr Leu
   -50                      -45                      -40

Ala Leu Trp Val Phe Val His Ile Pro Ser Ser Ser Thr Phe Ile Ile
   -35                      -30                      -25

Tyr Leu Lys Asn Thr Leu Val Ala Asp Leu Xaa Met Thr Leu Met Leu
   -20                      -15                      -10

Pro Phe Lys Ile Leu Ser Asp Ser His Leu Ala Pro Trp Gln Leu Arg
   -5                      1                      5                      10

Ala Phe Val Cys Arg Phe Ser Ser Val Ile Phe Tyr Glu Thr Met Tyr
   15                      20                      25

Val Gly Glu Gly
   30
  
```

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Spleen

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -46..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 6.3
 seq SIGVLTLSHLISG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```

Met Ser Ser Val Leu Ala Ala Ser His Pro Leu Val Leu Ser Ser Asn
  
```

-45

-40

-35

Ala Gly Thr Pro Gly Ile Ser Glu Lys Asp Asn Arg Asp Pro Ala Gly
 -30 -25 -20 -15

Ser Ser Ile Gly Val Leu Thr Leu Ser His Leu Ile Ser Gly Leu Arg
 -10 -5 1

Thr Leu Tyr Thr Leu Leu His Phe Pro Leu Arg
 5 10

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Thyroid

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -50..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq LIILGLVLFMVYG/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

Met Gly Leu Ala Met Glu His Gly Gly Ser Tyr Ala Arg Ala Gly Gly
 -50 -45 -40 -35

Ser Ser Arg Gly Cys Trp Tyr Tyr Leu Arg Tyr Phe Phe Leu Phe Val
 -30 -25 -20

Ser Leu Ile Gln Phe Leu Ile Ile Leu Gly Leu Val Leu Phe Met Val
 -15 -10 -5

Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn Leu Gln Ala Thr Glu
 1 5 10

Arg Arg Ala Glu Gly Leu Tyr Xaa Gln Leu Leu Gly Leu Thr Ala Ser
 15 20 25 30

Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr Thr Arg Ala Lys Asp
 35 40 45

Ala Ile Met Gln Met Trp Leu Asn Ala
 50 55

(1) INFORMATION FOR SEQ ID NO: 312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -64..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq SCLVSGWGLLANG/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 -60 -55 -50

Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 -45 -40 -35

Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 -30 -25 -20

Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly
 -15 -10 -5

Gln Arg
 1

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VICCVLFLLFILG/YI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

```

Met Gly Gly Lys Gln Arg Asp Glu Asp Asp Glu Ala Tyr Gly Lys Pro
   -45                               -40                       -35
Val Lys Tyr Asp Pro Ser Phe Arg Gly Pro Ile Lys Asn Arg Ser Cys
   -30                               -25                       -20
Thr Asp Val Ile Cys Cys Val Leu Phe Leu Leu Phe Ile Leu Gly Tyr
   -15                               -10                       -5                       1
Ile Val Val Gly Ile Val Ala Trp Leu Tyr Gly Asp Pro Arg Gln Val
                   5                               10                       15
Leu Tyr Pro Arg Asn Ser Thr Gly Ala Tyr Cys Gly Met Gly Glu Asn
   20                               25                               30
Lys Asp Lys Pro Tyr Leu Leu Tyr Phe Asn Ile Phe Ser Cys Ile Leu
   35                               40                               45
Ser Ser Asn Ile Ile Ser Val Ala Glu Asn Gly Leu Gln Cys Pro Thr
   50                               55                               60                       65
Pro Gln Val Cys Val Ser Ser Cys Pro Glu Asp Pro Trp Thr Xaa Xaa
                   70                               75                       80
Lys Thr Ser Ser His Arg Leu Leu Gly Lys Ser Ser Ile Gln
   85                               90                               95

```

(2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.3
seq VLLFLAWVCFLFY/AG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

```

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe Leu
   -15                               -10                       -5
Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu Thr Arg
   1                               5                               10
Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro Gly Pro Gly
   15                               20                               25                       30

```

Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala Cys Trp Met Ala
 35 40 45

Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile Asp Ala Leu Arg Phe
 50 55 60

Asp Phe Ala Gln Pro Gln His Ser His Val Pro Arg Glu Pro Pro Val
 65 70 75

Ser Leu Pro Phe Leu Gly Lys Leu Ser Ser Leu Gln Arg Ile Leu Glu
 80 85 90

Ile Gln Pro His His Ala Arg Leu
 95 100

(2) INFORMATION FOR SEQ ID NO: 315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -81..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.7
seq CWMMLLGSGXSFL/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

Met Ser Pro Val Leu His Phe Tyr Val Arg Pro Ser Gly His Glu Gly
 -80 -75 -70

Ala Ala Ser Gly His Thr Arg Arg Lys Leu Gln Gly Lys Leu Pro Glu
 -65 -60 -55 -50

Leu Gln Gly Val Glu Thr Glu Leu Cys Tyr Asn Val Asn Trp Thr Ala
 -45 -40 -35

Glu Ala Leu Pro Ser Ala Glu Glu Thr Lys Lys Leu Met Trp Leu Phe
 -30 -25 -20

Gly Cys Pro Tyr Cys Trp Met Met Leu Leu Gly Ser Xaa Gly Ser Phe
 -15 -10 -5

Leu Ala Pro Met Thr Cys Xaa Trp Arg Ser
 1 5

(2) INFORMATION FOR SEQ ID NO: 316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq ILRLLGSLSNAYS/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
-35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser
-20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met
1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp
15 20 25

Pro Ser Asn Met Tyr Thr Lys Tyr Tyr Ile His Arg Asn Gly
30 35 40

(2) INFORMATION FOR SEQ ID NO: 317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq LLRVLNLPNHSIG/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

Met Met Gly Val Ala Lys Leu Thr Leu Leu Arg Val Leu Asn Leu Pro
 -20 -15 -10

His Asn Ser Ile Gly Cys Val Glu Gly Leu Lys Glu Leu Val His Leu
 -5 1 5 10

Glu Trp Leu Asn Leu Ala Gly Asn Asn Leu Lys Ala Met Glu Gln Xaa
 15 20 25

Asn Ser Cys Thr Ala Leu Gln His Leu Asp
 30 35

(2) INFORMATION FOR SEQ ID NO: 318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.6
seq ILRLLGSLSNAYS/PR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Asp Val Thr Pro Arg Glu Ser Leu Ser Ile Leu Val Val Ala Gly
 -35 -30 -25

Ser Gly Gly His Thr Thr Glu Ile Leu Arg Leu Leu Gly Ser Leu Ser
 -20 -15 -10 -5

Asn Ala Tyr Ser Pro Arg His Tyr Val Ile Ala Asp Thr Asp Glu Met
 1 5 10

Ser Ala Asn Lys Ile Asn Ser Phe Glu Leu Asp Arg Ala Asp Arg Asp
 15 20 25

Arg

(2) INFORMATION FOR SEQ ID NO: 319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Colon

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -13..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.5
seq MVLLTMIARVADG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

Met Val Leu Leu Thr Met Ile Ala Arg Val Ala Asp Gly Leu Pro Leu
-10 -5 1
Ala Ala Ser Met Gln Glu Glu Val Arg Thr Ala Pro Arg Ala Leu
5 10 15

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -47..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 5.3
seq GCGMFTFLSSVXA/AV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
-45 -40 -35
Gly Thr Ala Val Glu Thr Glu Gly Xaa Gly Ser Arg His Pro Pro Trp
-30 -25 -20
Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Xaa Ala Ala
-15 -10 -5 1
Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
5 10 15
Leu Leu Gln Ile Lys Thr Leu Leu Ala Xaa Ser Cys His Glu Gln Glu

20

25

30

Met Val Val Ser Ser Leu Val Ile Gly .
35 40

(2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.2
seq LLFPVGRSWSCFA/QT

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

Met Glu Thr Phe Leu Glu Pro Asn Asn Lys Lys Leu Leu Phe Pro Val
-20 -15 -10

Gly Arg Ser Trp Ser Cys Phe Ala Gln Thr Xaa Ser Leu Ala Lys Tyr
-5 1 5

Ile Pro Tyr Ser Leu Trp Lys Tyr Ser Val Leu Ser Gly His Ser
10 15 20

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq FLWGLALPLFFFC/WE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

```

Met Gly Phe Leu Trp Gly Leu Ala Leu Pro Leu Phe Phe Phe Cys Trp
-15          -10          -5          1
Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg Arg Ala
          5          10          15
Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala Met Thr Leu
          20          25          30
Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu Ser Ala Glu Thr
          35          40          45
Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Val Pro Glu Ala Glu Thr
          50          55          60          65
Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg Glu Thr Arg Ser Phe Thr
          70          75          80
Lys Thr Xaa Pro Asn Phe Met Val Leu Xaa Xaa Xaa Val Thr
          85          90          95

```

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq WLLSDILGQGATA/NV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

```

Met Gln Ser Thr Ser Asn His Leu Trp Leu Leu Ser Asp Ile Leu Gly
-20          -15          -10
Gln Gly Ala Thr Ala Asn Val Phe Arg Gly Arg His Lys Lys Thr Gly
-5          1          5          10
Asp Leu Phe Ala Ile Lys Val Phe Asn Asn Ile Ser Phe Leu Arg Pro
          15          20          25
Val Asp Val Gln Met Arg Glu Phe Glu Val Leu Lys Lys Leu Asn His
          30          35          40

```

Lys Asn Ile Val Lys Leu Phe Ala Ile Glu Glu Glu Thr Gly
45 50 55

(2) INFORMATION FOR SEQ ID NO: 324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.9
seq ICAGSVLPPYSNC/QM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

Met Val Glu Ile Cys Ala Gly Ser Val Leu Pro Pro Tyr Ser Asn Cys
-15 -10 -5

Gln Met Pro Glu Pro Ser Ile Phe Thr Leu Ile His Phe His Thr Tyr
1 5 10 15

Tyr Cys Leu Thr Thr Pro Gln
20

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -43..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq LLAFGTSCSVVXY/XP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

Met Val Ala Pro Val Leu Glu Thr Ser His Val Phe Cys Cys Pro Asn
 -40 -35 -30

Arg Val Arg Gly Val Leu Asn Trp Xaa Ser Gly Pro Arg Gly Leu Leu
 -25 -20 -15

Ala Phe Gly Thr Ser Cys Ser Val Val Xaa Tyr Xaa Pro Leu Xaa Arg
 -10 -5 1 5

Val Val Val Thr Xaa Leu Xaa Gly His Thr Ala Arg Val Asn Cys Ile
 10 15 20

Gln Trp Ile Xaa Lys Gln Xaa Gly Met
 25 30

(2) INFORMATION FOR SEQ ID NO: 326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.7
seq QLLLATLQEAATT/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly Ala
 -70 -65 -60 -55

Xaa Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro Gly Glu
 -50 -45 -40

Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln Asp Pro Arg
 -35 -30 -25

Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu Leu Ala Thr Leu
 -20 -15 -10

Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala Trp Arg Lys Asn Trp
 -5 1 5 10

Met Val Gly Gly Glu Gly Gly Ala Thr Gly Xaa His Arg Glu Thr Gly
 15 20 25

Leu Ala Ser Val Gly Ala Gly Pro Trp Leu Gly Arg Arg Asn Pro Arg
 30 35 40

Gln Leu Ser Pro Ser
45

(2) INFORMATION FOR SEQ ID NO: 327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq LLPFGMLCASSTT/KC

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Arg Gln Thr Leu Pro Cys Ile Tyr Phe Trp Gly Gly Leu Leu Pro
-25 -20 -15

Phe Gly Met Leu Cys Ala Ser Ser Thr Thr Lys Cys Thr Val Ser His
-10 -5 1 5

Glu Val Ala Asp Cys Ser His Leu Lys Leu Thr Gln Val Pro Asp Asp
10 15 20

Leu Pro Thr Asn Ile Thr Val Leu Asn Leu Thr His Asn Gln Leu Arg
25 30 35

Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu
40 45 50

Asp Val Gly Phe Asn Thr Ile Ser Lys Leu Glu
55 60 65

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -110..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.6
seq HTXGLLGFRXQG/SI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

```

Met Ala Asp Asp Leu Glu Gln Gln Ser Gln Gly Trp Leu Ser Ser Trp
-110                               -105                   -100                   -95
Leu Pro Thr Trp Arg Pro Thr Ser Met Ser Gln Leu Lys Asn Val Glu
                               -90                   -85                   -80
Ala Arg Ile Leu Gln Cys Leu Gln Asn Lys Phe Leu Ala Arg Tyr Val
                               -75                   -70                   -65
Ser Leu Pro Asn Gln Asn Lys Ile Trp Thr Val Thr Val Ser Pro Glu
                               -60                   -55                   -50
Gln Asn Asp Arg Thr Pro Leu Val Met Val His Gly Phe Gly Gly Gly
-45                               -40                   -35
Val Gly Leu Trp Ile Leu Asn Met Asp Ser Leu Xaa Ala Arg Arg Thr
-30                               -25                   -20                   -15
Leu His Thr Xaa Gly Leu Leu Gly Phe Gly Arg Xaa Gln Gly Ser Ile
                               -10                   -5                   1
Pro Lys Gly Pro Glu Gly Leu Xaa Asp Glu Phe Val Xaa Ser Ile Xaa
                               5                   10                   15
Thr Trp Arg Glu Thr Trp
20

```

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Large intestine

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.5
seq PLSMILLSDKIQS/SK

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:


```

Met Lys Val Thr Gly Ile Thr Ile Leu Phe Trp Pro Leu Ser Met Ile
      -20                      -15                      -10

Leu Leu Ser Asp Lys Ile Gln Ser Ser Lys Arg Glu Val Gln Cys Asn
      -5                      1                      5

Phe Thr Glu Lys Asn Tyr Thr Leu Ile Pro Ala Asp Ile Lys Lys Asp
      10                      15                      20

Val Thr Ile Leu Asp Leu Ser Tyr Asn Gln Xaa Thr Leu Asn Gly Thr
      25                      30                      35                      40

Asp Thr

```

(2) INFORMATION FOR SEQ ID NO: 330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -96..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.4
seq HLSWSSSAYQAWA/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

```

Met Ala Ala Gly Arg Ala Gln Val Pro Ser Ser Glu Gln Ala Trp Leu
      -95                      -90                      -85

Glu Asp Ala Gln Val Phe Ile Gln Lys Thr Leu Cys Pro Ala Val Lys
      -80                      -75                      -70                      -65

Glu Pro Asn Val Gln Leu Thr Pro Leu Val Ile Asp Cys Val Lys Thr
      -60                      -55                      -50

Val Trp Leu Ser Gln Gly Arg Asn Gln Gly Ser Thr Leu Pro Leu Ser
      -45                      -40                      -35

Tyr Ser Phe Val Ser Val Gln Asp Leu Lys Thr His Gln Arg Leu Pro
      -30                      -25                      -20

Cys Cys Ser His Leu Ser Trp Ser Ser Ser Ala Tyr Gln Ala Trp Ala
      -15                      -10                      -5

Gln Glu Ala Gly Pro Asn Gly Asn Pro Pro Gly
      1                      5                      10

```

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -14...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4
seq STCCWCTPGGAST/ID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

Met Ser Thr Cys Cys Trp Cys Thr Pro Gly Gly Ala Ser Thr Ile Asp
 -10 -5 1
Phe Leu Lys Arg Tyr Ala Ser Asn Thr Pro Ser Gly Glu Phe Gln Thr
 5 10 15
Ala Asp Glu Asp Leu Cys Tyr Cys Leu Gly
 20 25

(2) INFORMATION FOR SEQ ID NO: 332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq VVEILPYLPCLTA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

Met Pro Phe Ala Glu Asp Lys Thr Tyr Lys Tyr Ile Cys Arg Asn Phe

-35

-30

-25

Ser Asn Phe Cys Xaa Val Asp Val Val Glu Ile Leu Pro Tyr Leu Pro
 -20 -15 -10 -5

Cys Leu Thr Ala Arg Asp Gln Asp Arg Leu Arg Ala Thr Cys Thr Leu
 1 5 10

Ser Gly Asn Arg Ala
 15

(2) INFORMATION FOR SEQ ID NO: 333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -107..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.9
seq IVLVLLLLGRYTEE/EQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

Met Ala Glu Ser Glu Asp Arg Ser Leu Arg Ile Val Leu Val Gly Lys
 -105 -100 -95

Thr Gly Ser Gly Lys Ser Ala Thr Ala Asn Thr Ile Leu Gly Glu Glu
 -90 -85 -80

Ile Phe Asp Ser Arg Ile Ala Ala Gln Ala Val Thr Lys Asn Cys Gln
 -75 -70 -65 -60

Lys Ala Ser Arg Glu Trp Gln Gly Arg Asp Leu Leu Val Val Asp Thr
 -55 -50 -45

Pro Gly Leu Phe Asp Thr Lys Glu Ser Leu Xaa Thr Thr Cys Lys Glu
 -40 -35 -30

Ile Xaa Arg Cys Ile Ile Ser Ser Cys Pro Gly Pro His Ala Ile Val
 -25 -20 -15

Leu Val Leu Leu Leu Gly Arg Tyr Thr Glu Glu Glu Gln Lys Thr Val
 -10 -5 1 5

Ala Leu Ile Xaa Leu
 10

(2) INFORMATION FOR SEQ ID NO: 334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -49..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.8
seq LLXCVGNFFGSTQ/DA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

```

Met Ala Gln Lys  Pro Leu Arg Leu Leu Ala Cys Gly Asp Val Glu Gly
      -45                -40                -35

Lys Phe Asp Ile  Leu Phe Asn Arg Val Gln Ala Ile Gln Lys Xaa Ser
      -30                -25                -20

Gly Asn Phe Asp Leu Leu Xaa Cys Val Gly Asn Phe Phe Gly Ser Thr
      -15                -10                -5

Gln Asp Ala Glu Trp Glu Glu Tyr Lys Thr Gly Ile Lys Lys Ala Pro
      1                5                10                15

Ile Gln Thr Tyr Val Leu Gly Ala Asn Asn Gln Glu Thr Val Lys Tyr
      20                25                30

Phe Gln Asp Ala Asp Gly Cys Glu Leu Ala Glu Asn Ile Thr Tyr Leu
      35                40                45

Gly Arg Gly
      50

```

(2) INFORMATION FOR SEQ ID NO: 335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -52..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RPVLLHLHQTAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

```

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Leu Trp Lys Met
   -50                      -45                      -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
   -35                      -30                      -25

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
   -20                      -15                      -10                      -5

Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
                   1                      5                      10

Gln Gln Leu Phe Pro Gln Trp His Leu Pro Ile Lys Ile Ala Ala Ile
   15                      20                      25

Ile Ala Xaa Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Val Xaa His
   30                      35                      40

Pro Leu Ala Thr Ser His Gln Gln Tyr Phe Tyr Lys Ile
   45                      50                      55
  
```

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids
 (B) TYPE: AMINO ACID
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
 (F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
 (B) LOCATION: -52..-1
 (C) IDENTIFICATION METHOD: Von Heijne matrix
 (D) OTHER INFORMATION: score 3.8
 seq RPVLLHLHQTAHA/DE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

```

Met Glu Ser Arg Lys Asp Ile Thr Asn Gln Glu Glu Xaa Trp Lys Met
   -50                      -45                      -40

Lys Pro Arg Arg Asn Leu Glu Glu Asp Asp Tyr Leu His Lys Asp Thr
   -35                      -30                      -25
  
```

Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Leu His Leu His Gln
 -20 -15 -10 -5
 Thr Ala His Ala Asp Glu Phe Asp Cys Pro Ser Glu Leu Gln His Thr
 1 5 10
 Gln Gly

(2) INFORMATION FOR SEQ ID NO: 337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq STLASVPPAATFG/AD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn Tyr Phe Ser
 -35 -30 -25
 Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val Pro Pro Ala
 -20 -15 -10 -5
 Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser Asn Pro Gln
 1 5 10
 Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly Glu Gln Pro
 15 20 25
 Gln Xaa Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser Tyr Gln Val
 30 35 40
 Glu Lys Asn Lys Tyr Asp Ala Thr Gly
 45 50

(2) INFORMATION FOR SEQ ID NO: 338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Muscle

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -58..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LVSFVAVSSEGTEQ/GE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

Met Arg Asp Cys Pro Gly Val Glu Xaa Ile Leu Asp Cys Ser Xaa Arg
-55 -50 -45
Gln Lys Thr Glu Gly Cys Arg Leu Gln Ala Gly Lys Glu Cys Val Asp
-40 -35 -30
Ser Pro Val Glu Gly Gly Gln Ser Glu Ala Pro Pro Ser Leu Val Ser
-25 -20 -15
Phe Ala Val Ser Ser Glu Gly Thr Glu Gln Gly Glu Asp Pro Arg Ser
-10 -5 1 5
Glu Lys Asp His Ser Arg Pro His Lys His Arg Ala Arg His Ala Arg
10 15 20
Leu Arg Arg Ser Glu Ser Leu Ser Xaa Lys Gln Val Lys Glu Ala Lys
25 30 35
Ser Xaa Cys Lys Ser Ile Ala Leu Leu Leu Thr Asp Ala Pro Xaa Pro
40 45 50
Asn Ser Lys Gly Val Leu Met Phe Lys Lys Arg
55 60 65

(2) INFORMATION FOR SEQ ID NO: 339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -37..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq LVFNFLILILT/1W

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

```

Met Glu Arg Gln Ser Arg Val Met Ser Glu Lys Asp Glu Tyr Gln Phe
  -35                      -30                      -25
Gln His Gln Gly Ala Val Glu Leu Leu Val Phe Asn Phe Leu Leu Ile
  -20                      -15                      -10
Leu Thr Ile Leu Thr Ile Trp Leu Phe Lys Asn His Arg Phe Arg Phe
  -5                      1                      5                      10
Leu His Glu Thr Gly Gly Ala Met Val Tyr
          15                      20

```

(2) INFORMATION FOR SEQ ID NO: 340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.4
seq SLLLVQLLTPCSA/QF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

```

Met Lys Met Ala Ser Ser Leu Ala Phe Leu Leu Leu Asn Phe His Val
          -25                      -20                      -15
Ser Leu Leu Leu Val Gln Leu Leu Thr Pro Cys Ser Ala Gln Phe Ser
          -10                      -5                      1
Val Leu Xaa Xaa Ser Gly Pro Ile Leu Ala Met Val Gly Glu Asp Ala
          5                      10                      15
Asp Leu
20

```

(2) INFORMATION FOR SEQ ID NO: 341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -32..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 12.6
seq LLALLTVSTPSWC/QS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

Met Val Phe Leu Pro Leu Lys Trp Ser Leu Ala Thr Met Ser Phe Leu
-30 -25 -20

Leu Ser Ser Leu Leu Ala Leu Leu Thr Val Ser Thr Pro Ser Trp Cys
-15 -10 -5

Gln Ser Thr Glu Ala Ser Pro Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO: 342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -26..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.8
seq SLLLLLLXCVHWS/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:

Met Glu Ser Ala Ala Ala Leu His Phe Ser Arg Pro Ala Ser Leu Leu
-25 -20 -15

Leu Leu Leu Leu Xaa Cys Val His Trp Ser Gln Pro Ser Leu Leu Ser
-10 -5 1 5

Trp

(2) INFORMATION FOR SEQ ID NO: 343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig peptide

(B) LOCATION: -20..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 11.2
seq AFLLLVALSYTLA/RD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(3) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -46..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.3
seq LVLLLVLTLCSL/VP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:

```

Met Gly Pro Trp Gly Glu Pro Glu Leu Leu Val Trp Arg Pro Glu Ala
-45                      -40                      -35

Val Ala Ser Glu Pro Pro Val Pro Val Gly Leu Glu Val Lys Leu Gly
-30                      -25                      -20                      -15

Ala Leu Val Leu Leu Leu Val Leu Thr Leu Leu Cys Ser Leu Val Pro
                      -10                      -5                      1

Ile Cys Val Leu Arg Arg Pro Gly Ala Asn His Glu Gly Ser Ala Ser
      5                      10                      15

Arg Gln Lys Ala Leu Ser Pro Lys
  20                      25

```

(2) INFORMATION FOR SEQ ID NO: 345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.1
seq LLLQLAVLGAALA/AA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```

Met Ala Pro Leu Leu Leu Gln Leu Ala Val Leu Gly Ala Ala Leu Ala
-15                      -10                      -5

Ala Ala Ala Leu Val Leu Ile Ser Ile Val Ala Phe Thr Thr Ala Thr
  1                      5                      10                      15

Lys Met Pro Ala Leu His Arg His Glu Glu Glu Lys Phe Phe Leu Asn
      20                      25                      30

Ala Lys Gly Gln Lys Glu Thr Leu Pro Ser Ile Trp Asp Ser Pro Thr
      35                      40                      45

```

Lys Gln Leu Ser Val Val Val Pro Ser Tyr Asn Glu Glu Lys Arg Leu
 50 55 60
 Pro Val Met Met Asp Glu Ala Leu Ser Tyr Leu Glu Lys Arg Gln Lys
 65 70 75 80
 Arg Asp Pro Ala Phe Thr Tyr Glu Val Ile Val Val Asp Asp Gly Ser
 85 90 95
 Lys Asp Gln Thr Ser Lys
 100

(2) INFORMATION FOR SEQ ID NO: 346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -27..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.8
seq SALLVGFLSVIFA/LV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

Met Ala Met Glu Gly Tyr Trp Arg Phe Leu Xaa Leu Leu Gly Ser Ala
 -25 -20 -15
 Leu Leu Val Gly Phe Leu Ser Val Ile Phe Ala Leu Val Trp Val Leu
 -10 -5 1 5
 His Tyr Arg Glu Gly Leu Gly Trp Asp Gly Ser Ala Leu Glu Phe Asn
 10 15 20
 Trp Xaa Pro Val Leu Met Val Thr Gly Phe Val Phe Ile Gln Gly Ile
 25 30 35
 Ala Ile Ile Val Tyr Arg Leu Pro Trp Thr Trp Lys Cys Ser Lys Leu
 40 45 50
 Leu Met Lys Ser Ile His Ala Xaa Leu Asn Ala Val Ala Ala Ile Leu
 55 60 65
 Ala Ile Ile Ser Val Val Ala Val Phe Glu Asn His Asn Val Asn Asn
 70 75 80 85
 Ile Ala Asn Met Tyr Ser Leu His Ser Trp Val Gly Leu Ile Ala
 90 95 100

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -17..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq LALSLILVLAFG/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
-15 -10 -5

Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
1 5 10 15

Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
20 25 30

Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
35 40 45

Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
50 55 60

Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
65 70 75

Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
80 85 90 95

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -15..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.4
seq AMWLLCVALAVLA/WG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Glu Ala Met Trp Leu Leu Cys Val Ala Leu Ala Val Leu Ala Trp
-15 -10 -5 1

Gly Phe Leu Trp Val Trp Asp Ser Ser Glu Arg Met Lys Ser Arg Glu
5 10 15

Gln Gly Xaa Arg Leu Gly Ala Glu Ser Arg Thr Leu Leu Val Ile Ala
20 25 30

His Pro Asp Asp Glu Ala Met Trp
35 40

(2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: -38..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 7.8
seq LVFTVSLFAWICC/QR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Ala Pro Ile Thr Thr Ser Arg Glu Glu Phe Asp Glu Ile Pro Thr
-35 -30 -25

Val Val Gly Ile Phe Ser Ala Phe Gly Leu Val Phe Thr Val Ser Leu
-20 -15 -10

Phe Ala Trp Ile Cys Cys Gln Arg Lys Ser Ser Lys Ser Asn Lys Thr
-5 1 5 10

Pro Pro Tyr Lys Phe Val His Val Leu Xaa Gly Val Asp Ile Tyr Pro
15 20 25

Glu Asn Leu Asn Ser Lys Lys Lys
30

(2) INFORMATION FOR SEQ ID NO: 350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -18..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 7.4
seq GWLVLCVLAISLA/SM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Glu Gly Pro Arg Gly Trp Leu Val Leu Cys Val Leu Ala Ile Ser
-15 -10 -5

Leu Ala Ser Met Val Thr Glu Asp Leu Cys Arg Ala Pro Asp Gly Lys
1 5 10

Lys Gly Glu Ala Gly Arg Pro Gly Arg Arg Gly Arg Pro Gly Leu Lys
15 20 25 30

Gly Glu Gln Gly Glu Pro Gly Ala Pro Gly Ile Arg Thr Gly Ile Gln
35 40 45

Gly Leu Lys Gly Asp Gln Gly Glu Pro Gly Pro Ser Gly Asn Pro Gly
50 55 60

Lys Val Gly Tyr Pro Gly Pro Ser Gly Pro Leu Gly Ala Arg Gly Ile
65 70 75

Pro Gly Ile Lys Gly Thr Lys Gly Ser Pro Gly Asn Ile Lys Asp Gln
30 85 90

Pro Arg Pro Ala Phe Ser Ala Ile Arg
95 100

(2) INFORMATION FOR SEQ ID NO: 351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -63..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2
seq VLLTLLLI AFIFL/II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met	Thr	Ala	Trp	Glu	Ala	Met	Ala	Pro	His	Val	Asn	Pro	Thr	Leu	Lys	
			-60					-55						-50		
Asp	Lys	Ala	Leu	Ser	Pro	Gln	Gln	Xaa	Xaa	Xaa	Thr	Ser	Pro	Ala	Pro	
		-45					-40						-35			
Cys	Xaa	Ser	Asn	His	His	Asn	Lys	Lys	His	Leu	Ile	Leu	Ala	Phe	Cys	
	-30					-25					-20					
Ala	Gly	Val	Leu	Leu	Thr	Leu	Leu	Leu	Ile	Ala	Phe	Ile	Phe	Leu	Ile	
-15					-10				-5						1	
Ile	Lys	Ser	Tyr	Arg	Lys	Tyr	His	Ser	Lys	Pro	Gln	Ala	Pro	Gly		
		5						10						15		

(2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -18..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1
seq LLCECLLLXAGYA/HD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Leu Cys Ser Leu Leu Leu Cys Glu Cys Leu Leu Leu Xaa Ala Gly
-15 -10 -5
Tyr Ala His Asp Asp Asp Trp Ile Asp Pro Thr Asp Met Leu Asn Tyr
1 5 10
Asp Ala Ala Ser Gly Thr Met Arg Lys Ser Gln Ala Lys Tyr Gly Ile
15 20 25 30
Ser Gly Glu Lys Asp Val Ser Pro Asp Leu Ser Cys Ala Xaa Glu Ile
35 40 45
Ser Glu

(2) INFORMATION FOR SEQ ID NO: 353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.9
seq LVXSLPVHCLTFA/SS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

Met Gly His Ala Met Gly Leu Val Xaa Ser Leu Pro Val His Cys Leu
-15 -10 -5
Thr Phe Ala Ser Ser Ala Pro Ser Ser Pro Gln Pro Thr Arg Met Trp
1 5 10
Phe Xaa Ala Gln Ala His Xaa Pro Pro Leu Ile Leu Gly Pro
15 20 25

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -16..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.7
seq CFSLVLLLSIWT/TR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

Met Ala Arg Cys Phe Ser Leu Val Leu Leu Leu Thr Ser Ile Trp Thr
-15 -10 -5
Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
1 5 10 15
Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
20 25 30
Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
35 40 45
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
50 55 60
Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
65 70 75 80
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
85 90 95
Val Leu Ile Trp
100

(2) INFORMATION FOR SEQ ID NO: 355:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: -59..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 6.6
seq VLAQLAFLSQISQ/CI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

Met Leu Leu Thr Arg Lys Gln Thr Cys Gln Leu Gly Ile Leu Leu Ser
 -55 -50 -45

Ile His Arg Gln His Ser Lys Asp Leu Gln Asp Ile Val Ala Thr Leu
 -40 -35 -30

Gly Pro Arg Ser Ala Thr His Pro His Gln Pro Ala Ile Gln Val Leu
 -25 -20 -15

Ala Gln Leu Ala Phe Leu Ser Gln Ile Ser Gln Cys Ile Ile Ser Gln
 -10 -5 1 5

Arg

(2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -28..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 6.6
seq IVSLLGFVATVTL/IP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Trp Ala Phe Ser Glu Leu Pro Met Pro Leu Leu Ile Asn Leu Ile
 -25 -20 -15

Val Ser Leu Leu Gly Phe Val Ala Thr Val Thr Leu Ile Pro Ala Phe
 -10 -5 1

Arg Gly His Phe Ile Ala Ala Arg Leu Cys Gly Gln Asp Leu Asn Lys
 5 10 15 20

Thr Ser Arg Gln Gln Ile Pro Glu Ser Gln Gly Val Ile Ser Gly Ala
 25 30 35

Val Phe Leu Ile Ile Leu Phe Cys
 40

(2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -23...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq PASLSLLTFKVYA/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Phe Lys Val Ile Gln Arg Ser Val Gly Pro Ala Ser Leu Ser Leu
-20 -15 -10
Leu Thr Phe Lys Val Tyr Ala Ala Pro Lys Lys Asp Ser Pro Pro Lys
-5 1 5
Asn Ser Val Lys Val Asp Glu Leu Ser Leu Tyr Ser Val Pro Glu Gly
10 15 20 25
Gln Ser Lys Tyr Val Glu Glu Ala Arg Ser Gln Leu Glu Glu Ser Ile
30 35 40
Ser Gln Leu Arg His Tyr Cys Glu Pro Tyr Thr Thr Trp Cys Gln Glu
45 50 55
Thr Tyr

(2) INFORMATION FOR SEQ ID NO: 358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -136...-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.4
seq LISVALVQGWALG/GG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Ala Lys Ser Leu Leu Lys Thr Ala Ser Leu Ser Gly Arg Thr Lys
 -135 -130 -125

Leu Leu His Gln Thr Gly Leu Ser Leu Tyr Ser Thr Ser His Gly Phe
 -120 -115 -110 -105

Tyr Glu Glu Glu Val Lys Lys Thr Leu Gln Gln Phe Pro Gly Gly Ser
 -100 -95 -90

Ile Asp Leu Gln Lys Glu Asp Asn Gly Ile Gly Ile Leu Thr Leu Asn
 -85 -80 -75

Asn Pro Ser Arg Met Asn Ala Phe Ser Gly Val Met Met Leu Gln Leu
 -70 -65 -60

Leu Glu Lys Val Ile Glu Leu Glu Asn Trp Thr Glu Gly Lys Gly Leu
 -55 -50 -45

Ile Val Arg Gly Ala Lys Asn Thr Phe Ser Ser Gly Ser Asp Leu Asn
 -40 -35 -30 -25

Ala Val Lys Ser Leu Gly Leu Gln Arg Leu Pro Leu Ile Ser Val Ala
 -20 -15 -10

Leu Val Gln Gly Trp Ala Leu Gly Gly Gly Ala Ala
 -5 1

(2) INFORMATION FOR SEQ ID NO: 359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -44..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.3
seq PLLKILHAAGAQG/EM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Thr Ser Phe Ser Thr Ser Ala Gln Cys Ser Thr Ser Asp Ser Ala
 -40 -35 -30

Cys Arg Ile Ser Pro Gly Gln Ile Asn Xaa Val Arg Pro Lys Leu Pro
 -25 -20 -15

Leu Leu Lys Ile Leu His Ala Ala Gly Ala Gln Gly Glu Met Phe Thr

-10

-5

1

Val Lys Glu Val Met His Tyr Leu Gly Gln Tyr Ile Met Val Lys Gln
 5 10 15 20

(2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lung (cells)

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -112..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 5.1
seq AFAWLGVVPLTAC/RI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Asp Thr Ala Glu Glu Asp Ile Cys Arg Val Cys Arg Ser Glu Gly
 -110 -105 -100

Thr Pro Glu Lys Pro Leu Tyr His Pro Cys Val Cys Thr Gly Ser Ile
 -95 -90 -85

Lys Xaa Val His Gln Glu Cys Leu Val Gln Trp Leu Lys His Ser Arg
 -80 -75 -70 -65

Lys Glu Tyr Cys Glu Leu Cys Lys His Arg Phe Ala Phe Thr Pro Ile
 -60 -55 -50

Tyr Ser Pro Asp Met Pro Ser Arg Leu Pro Ile Gln Asp Ile Phe Ala
 -45 -40 -35

Gly Leu Val Thr Ser Ile Gly Thr Ala Ile Arg Tyr Trp Phe His Tyr
 -30 -25 -20

Thr Leu Val Ala Phe Ala Trp Leu Gly Val Val Pro Leu Thr Ala Cys
 -15 -10 -5

Arg Ile Tyr Lys Cys Leu Phe Thr Gly Ser Val Ser Ser Leu Leu Thr
 1 5 10 15

Leu Pro Leu Asp Met Leu Ser Thr Glu Asn Leu Leu Ala Asp Cys Leu
 20 25 30

Gln Gly Cys Phe Val Val Thr Cys Thr Leu Cys Ala Phe Ile
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.9
 seq MLIMLGIFNVHS/AV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu  
-10 -5 1

Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe Glu Xaa Gly Pro Gln  
5 10 15

Asn Ile Tyr Asn Leu Tyr Glu His Gly  
20 25

(2) INFORMATION FOR SEQ ID NO: 362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -112..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 4.5
                        seq AAVAVGMLXASYA/AV
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

Met Gly Gly Leu Trp Arg Pro Gly Trp Arg Cys Val Pro Phe Cys Gly
-110 -105 -100

Trp Arg Trp Ile His Pro Gly Ser Pro Thr Arg Ala Ala Glu Arg Val
 -95 -90 -85
 Glu Pro Phe Leu Arg Pro Glu Trp Ser Gly Thr Gly Gly Ala Glu Arg
 -80 -75 -70 -65
 Gly Leu Arg Trp Leu Gly Thr Trp Lys Arg Cys Ser Leu Arg Ala Arg
 -60 -55 -50
 His Pro Ala Leu Gln Pro Pro Arg Arg Pro Lys Ser Ser Asn Pro Phe
 -45 -40 -35
 Thr Arg Ala Xaa Glu Glu Glu Arg Arg Arg Xaa Asn Lys Thr Thr Leu
 -30 -25 -20
 Thr Tyr Val Ala Ala Val Ala Val Gly Met Leu Xaa Ala Ser Tyr Ala
 -15 -10 -5
 Ala Val
 1

(2) INFORMATION FOR SEQ ID NO: 363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -39..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 4.2
seq SDPLCVLFLNTSG/QQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

Met Ala Ala Gln Cys Val Thr Lys Val Ala Leu Asn Val Ser Cys Ala
 -35 -30 -25
 Asn Leu Leu Asp Lys Asp Ile Gly Ser Lys Ser Asp Pro Leu Cys Val
 -20 -15 -10
 Leu Phe Leu Asn Thr Ser Gly Gln Gln Trp Tyr Glu Val Glu Arg Thr
 -5 1 5
 Glu Arg Ile Lys Asn Cys Leu Asn Pro Gln Phe Ser Lys Thr Phe Ile
 10 15 20 25
 Ile Asp Tyr Tyr Phe Glu Val Val Gln Lys Leu Lys Phe Gly Val Tyr
 30 35 40

Asp Ile Xaa Asn Lys Thr Ile Glu Leu Ser Asp Asp Asp Phe Leu Gly
 45 50 55

(2) INFORMATION FOR SEQ ID NO: 364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -70..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.7
seq AVLDCAFYDPTHA/WS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro Pro Glu Asp Gly
 -70 -65 -60 -55

Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln Phe Leu Leu Val
 -50 -45 -40

Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val Pro Ala Asn Ser
 -35 -30 -25

Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu Asp Cys Ala Phe
 -20 -15 -10

Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp His Xaa Xaa Lys
 -5 1 5 10

Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val Gly Thr His Asp
 15 20 25

Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Ser
 30 35

(2) INFORMATION FOR SEQ ID NO: 365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -25..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.6
seq AHLWCWCGSHCCST/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Gly Lys His Leu Trp Tyr Pro Gly Gln Ala Ser Ala His Leu Cys
-25 -20 -15 -10
Trp Cys Gly Ser His Cys Cys Ser Thr Cys Val Phe Glu Asp Gln Leu
-5 1 5
Ser Asp Glu Arg Phe Gln Arg Ser Asn Ala Pro Ser Val Asn Ser Asp
10 15 20

(2) INFORMATION FOR SEQ ID NO: 366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -13..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 3.5
seq MLAVSLTVXLLGA/MM

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Leu Ala Val Ser Leu Thr Val Xaa Leu Leu Gly Ala Met Met Leu
-10 -5 1
Leu Glu Ser Pro Ile Asp Pro Gln Pro Leu Ser Phe Lys Glu Pro Pro
5 10 15
Leu Leu Leu Gly Val Leu His Pro Asn Thr Lys Leu Arg Gln Ala Glu
20 25 30 35
Arg Leu Phe Glu Asn Gln Leu Val Gly Pro Glu Ser Ile Ala His Ile
40 45 50

Gly Asp Val Met Phe Thr Gly Ser Trp
55 -60

(2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -76..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 3.5
seq MLELDLLVFHLWG/SQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Ser Ser Thr Leu Ala Lys Ile Ala Glu Ile Glu Ala Glu Met Ala
-75 -70 -65

Arg Thr Gln Lys Asn Lys Ala Thr Ala His His Leu Gly Leu Leu Lys
-60 -55 -50 -45

Ala Arg Leu Ala Lys Leu Arg Arg Glu Leu Ile Thr Pro Lys Gly Gly
-40 -35 -30

Gly Gly Gly Gly Pro Gly Glu Gly Phe Asp Trp Pro Arg Gln Val Met
-25 -20 -15

Leu Glu Leu Asp Leu Leu Val Phe His Leu Trp Gly Ser Gln His Cys
-10 -5 1

Leu Val Thr Trp Gln Gly
5 10

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -45..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.9
seq LVLALLLVSAALS/SV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

Met Ala Ala Ala Val Pro Lys Arg Met Arg Gly Pro Ala Gln Ala Lys
-45 -40 -35 -30
Leu Leu Pro Gly Ser Ala Ile Gln Ala Leu Val Gly Leu Ala Arg Pro
-25 -20 -15
Leu Val Leu Ala Leu Leu Leu Val Ser Ala Ala Leu Ser Ser Val Val
-10 -5 1
Ser Arg Thr Asp Ser Pro Ser Pro Leu
5 10

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -25..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 13.9
seq LLSLLFLVQGAHG/RG

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser Leu
-25 -20 -15 -10
Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu Asp Phe
-5 1 5
Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser Leu His Tyr
10 15 20
Lys Pro Thr Pro Xaa Leu Arg Ile Ser Ile Glu Asn Ser Glu Glu
25 30 35

(2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -88..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6
seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Met Val Val Gly Thr Gly Thr Ser Leu Ala Leu Ser Ser Leu Leu
 -85 -80 -75

Ser Leu Leu Leu Phe Ala Gly Met Gln Ile Tyr Ser Arg Gln Leu Ala
 -70 -65 -60

Ser Thr Glu Trp Leu Thr Ile Gln Gly Gly Leu Leu Gly Ser Gly Leu
 -55 -50 -45

Phe Val Phe Ser Leu Thr Ala Phe Asn Asn Leu Glu Asn Leu Val Phe
 -40 -35 -30 -25

Gly Lys Gly Phe Gln Ala Lys Ile Phe Pro Glu Ile Leu Leu Cys Leu
 -20 -15 -10

Leu Leu Ala Leu Phe Ala Ser Gly Leu Ile His Xaa Val Cys Val Thr
 -5 1 5

Thr Cys Phe Ile Phe Ser Arg Val Gly Leu Tyr Tyr Ile Asn Lys Ile
 10 15 20

Ser Ser Thr Leu Tyr Gln Ala Ala Ala Pro Val Leu Thr Pro Ala
 25 30 35

(2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6
seq VFCLLAVAPGAHS/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly
 -15 -10 -5

Ala His Ser Gln Glu Gln Leu Val Gln Ser Gly Ala Glu Val Leu Lys
 1 5 10

Pro Gly Ala Ser Val Asn Ile Ser Cys Arg Ala Ser Gly Phe Thr Phe
 15 20 25

Thr Asn Tyr Tyr Val His Trp Val Arg Gln Ala Pro Gly His Gly Leu
 30 35 40 45

Glu Trp Met Gly Val Ile Asn Pro Val Ser Gly Tyr Thr Ser Tyr Ala
 50 55 60

Gln Lys Leu Gln Gly Arg Leu Thr Met Thr Thr Asp Thr Ala Ala Asn
 65 70 75

Ile Val Tyr Met Asp Leu Ser Arg Leu Lys Ser Asp Asp Thr Ala Val
 80 85 90

Tyr Phe Cys Ala Lys Val Arg Cys Leu Lys Gly Ile Cys Tyr Thr Glu
 95 100 105

Asp Ala Leu Asp Leu Trp
110 115

(2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -113..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.6

seq ILLCLLLALFASG/LI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

```

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Ser Pro Phe Leu Ala Arg
      -110                      -105                      -100

Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly
      -95                      -90                      -85

Thr Ser Leu Ala Leu Xaa Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly
      -80                      -75                      -70

Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile
-65                      -60                      -55                      -50

Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala
      -45                      -40                      -35

Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys
      -30                      -25                      -20

Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser
      -15                      -10                      -5

Gly Leu Ile His Arg Val Cys Val Thr Thr Cys Phe Ile Phe Ser Met
      1                      5                      10                      15

Val Gly Leu Tyr Tyr Ile Asn Lys Ile Ser Ser
      20                      25

```

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Heart

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -24..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.4
seq LMSLLLVLPVVEA/VE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

```

Met Thr Ser Val Ser Thr Gln Leu Ser Leu Val Leu Met Ser Leu Leu
      -20                      -15                      -10

Leu Val Leu Pro Val Val Glu Ala Val Glu Ala Gly Asp Ala Ile Ala

```

-5

1

5

Leu Leu Leu Gly Val Val Leu Ser Ile Thr Gly Ile Val Pro Ala Trp
10 15 20

Gly Tyr Met His Gly
25

(2) INFORMATION FOR SEQ ID NO: 374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11.2
seq ILVVLMGLPLAQA/LD

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Thr Pro Leu Leu Thr Leu Ile Leu Val Val Leu Met Gly Leu Pro
-20 -15 -10 -5

Leu Ala Gln Ala Leu Asp Cys His Val Cys Xaa Tyr Asn Gly Asp Asn
1 5 10

Cys

(2) INFORMATION FOR SEQ ID NO: 375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 11

seq LLALSLLVLWTSP/AP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

```

Met Ala Leu Leu Leu Ala Leu Ser Leu Leu Val Leu Trp Thr Ser Pro
  -15                -10                -5

Ala Pro Thr Leu Ser Gly Thr Asn Asp Ala Glu Asp Cys Cys Leu Ser
  1              5              10              15

Val Thr Gln Lys Pro Ile Pro Gly Tyr Ile Val Arg Asn Phe His Tyr
      20                25                30

Leu Leu Ile Lys Asp Gly Cys Arg Val Pro Ala Val Val Phe Thr Thr
      35                40                45

Leu Arg Gly Arg Gln Leu Cys Ala Pro Pro Asp Gln Pro Trp Val Glu
      50                55                60

Arg Ile Ile Gln Arg Leu Gln Arg Thr Ser Ala Lys Met Lys Xaa Arg
      65                70                75                80

Ser Ser Xaa Pro Met Xaa Val Xaa Arg Glu Pro Glu Ser Glu Ser Ser
      85                90                95

Ile Val Asn Xaa Tyr Leu Xaa Gly Glu Arg Xaa Arg
      100                105

```

(2) INFORMATION FOR SEQ ID NO: 376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 10.5
seq RLLLLPLLLAVSG/LR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

```

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
  -20                -15                -10

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
  -5              1              5              10

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met

```

15							20					25				
Gly	Asp	Leu	Val	Leu	Thr	Val	Leu	Ile	Ala	Leu	Ala	Val	Tyr	Phe	Leu	
		30					35					40				
Gly	Arg	Leu	Val	Pro	Arg	Gly	Arg	Gly	Ala	Ala	Glu	Ala	Xaa	Thr	Arg	
	45					50					55					
Lys	Gln	Arg	Ile	Thr	Glu	Thr	Gly	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	
60					65					70					75	
Gln	Arg	Ser	Asp	Val	Tyr	Ser										
80																

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(D) DEVELOPMENTAL STAGE: Fetal
(F) TISSUE TYPE: kidney

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
(B) LOCATION: -24..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 10
seq LCRALCLFPRVFA/AE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LMCLSLCTAFALS/KP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

Met Asp Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe
 -15 -10 -5

Ala Leu Ser Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro
 1 5 10

Gln Leu Ser Asp Lys Val His Asn Asp Ala Gln Ser Phe Xaa Tyr Asp
 15 20 25

His Asp Ala Phe Leu Gly Ala Glu Glu Ala Lys Xaa Phe Asp Gln Leu
 30 35 40 45

Thr Pro Glu Glu Ser Lys Glu Arg Leu Gly Lys Ile Val Ser Lys Ile
 50 55 60

Asp Gly Asp Lys Asp Gly Phe Val Thr Val Asp Glu Leu Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -30..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.5
seq LLFLSQFCILSGG/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Gly Gly Val Arg Pro Leu Arg Gly Leu Arg Ala Leu Cys Arg
 -30 -25 -20 -15

Val Leu Leu Phe Leu Ser Gln Phe Cys Ile Leu Ser Gly Gly Glu Ser
 -10 -5 1

Thr Glu Ile Pro Pro Tyr Val Met Lys Cys Pro Ser Asn Gly Leu Cys
 5 10 15

Ser Arg Leu Pro Ala Asp Cys Ile Asp Ser Thr Thr Asn Phe Ser Cys
 20 25 30

Thr Tyr Gly Lys Pro Val Thr Phe Asp Cys Xaa Val Lys Pro Ser Val
 35 40 45 50

Thr Cys Val Asp Gln Asp Phe Lys Ser Gln Lys Xaa Phe Ile Ile Asn
 55 60 65

Met Thr Cys

(2) INFORMATION FOR SEQ ID NO: 380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILLLLGAHP/SP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
 -20 -15 -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
 -5 1 5 10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
 15 20 25

Gly Lys Asn Tyr Phe Ser Phe Gly Xaa Ile Leu Phe Arg Asn Thr Thr
 30 35 40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile

45 50 55
Xaa Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
60 65 70 75
Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg
80 85 90
Gly Leu Ser Gly Lys Trp
95

(2) INFORMATION FOR SEQ ID NO: 381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq LLWLALACSPVHT/XL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5
Val His Thr Xaa Leu Ser Lys Ser Asp Ala Xaa Lys Pro Pro Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO: 382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Muscle

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -16..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 9.3
seq LFVAIFAVPLILG/QE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

```

Met Asp Val Leu Phe Val Ala Ile Phe Ala Val Pro Leu Ile Leu Gly
  -15                      -10                      -5

Gln Glu Tyr Glu Asp Glu Glu Arg Leu Gly Glu Asp Glu Tyr Tyr Gln
  1                      5                      10                      15

Val Val Tyr Tyr Tyr Thr Val Thr Pro Ile Met Met Xaa Leu Gly Xaa
      20                      25                      30

Xaa Phe Thr Ile Asp Tyr Xaa Ile Phe Glu Ser Glu
      35                      40

```

(2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (E) TISSUE TYPE: Substantia nigra

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.3
seq VLPVILLLLLGARP/S?

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

```

Met Ala Ala Ala Ala Trp Leu Gln Val Leu Pro Val Ile Leu Leu Leu
  -20                      -15                      -10

Leu Gly Ala His Pro Ser Pro Leu Ser Phe Phe Ser Ala Gly Pro Ala
  -5                      1                      5                      10

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser
      15                      20                      25

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr
      30                      35                      40

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile
      45                      50                      55

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe
      60                      65                      70                      75

```

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu
80 85

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (D) DEVELOPMENTAL STAGE: Fetal
- (F) TISSUE TYPE: brain

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9.2
seq LLXLALACSPVHT/TL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

Met Arg Thr Leu Phe Asn Leu Leu Xaa Leu Ala Leu Ala Cys Ser Pro
-15 -10 -5

Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
1 5 10

Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
15 20 25

Gly Leu Val Val Thr Asp Gly
30 35

(2) INFORMATION FOR SEQ ID NO: 385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: -40..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 9

seq LLCLLHFSIVSVA/AX

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

[illegible]

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
(B) TYPE: AMINO ACID
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

- ```
(A) NAME/KEY: sig_peptide
(B) LOCATION: -29..-1
(C) IDENTIFICATION METHOD: Von Heijne matrix
(D) OTHER INFORMATION: score 8.9
 seq ALLIVCDVPSASA/QR
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

```
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val Val
 -25 -20 -15
```

```
Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln Arg Lys
 -10 -5 i
```

```
Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met Glu Trp Thr
 5 10 15
```

```
Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys Phe Arg Arg Leu
 20 25 30 35
```

```
Val Lys Pro His Met
 40
```



## (2) INFORMATION FOR SEQ ID NO: 387:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq SAVLSGFVLGALA/FQ

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

```

Met Glu Gly Glu Ser Thr Ser Ala Val Leu Ser Gly Phe Val Leu Gly
 -15 -10 -5

Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu Gly Phe
 1 5 10

Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile Thr Asp Ser
 15 20 25

Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp Ile Gln Lys Tyr
 30 35 40 45

Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn Ser Ser Gly Glu Val
 50 55 60

Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser Asn Val Lys Lys Asn Val
 65 70 75

Val Gly Trp Tyr Lys Phe Arg Arg His Ser Asp Gln Ile Met Thr Phe
 80 85 90

Arg Glu Arg Leu Leu His Lys Asn Leu Gln Glu His Phe Ser Asn Gln
 95 100 105

Asp Leu Val Phe Leu Leu Leu Thr Pro
110 115

```

## (2) INFORMATION FOR SEQ ID NO: 388:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Hypertrophic prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.8  
seq VPMLLLIVGGSFG/LR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu  
-30 -25 -20  
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly  
-15 -10 -5  
Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met  
1 5 10 15  
Asp Pro Glu Arg  
20

## (2) INFORMATION FOR SEQ ID NO: 389:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -136..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.7  
seq AVALSLFLGWLGA/DR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

Met Ala Ala Ala Trp Xaa Ser Gly Pro Ser Ala Pro Glu Ala Val Thr  
-135 -130 -125  
Ala Arg Leu Val Gly Val Leu Trp Phe Val Ser Val Thr Thr Gly Pro  
-120 -115 -110 -105  
Trp Gly Ala Val Ala Thr Ser Ala Gly Gly Glu Glu Ser Leu Lys Cys  
-100 -95 -90

Glu Asp Leu Lys Val Gly Gln Tyr Ile Cys Lys Asp Pro Lys Ile Asn  
                     -85                    -80                    -75  
 Asp Ala Thr Gln Glu Pro Val Asn Cys Thr Asn Tyr Thr Ala His Val  
                     -70                    -65                    -60  
 Ser Cys Phe Pro Ala Pro Asn Ile Thr Cys Lys Asp Ser Ser Gly Asn  
                     -55                    -50                    -45  
 Glu Thr His Phe Thr Gly Asn Glu Val Gly Phe Phe Lys Pro Ile Ser  
                     -40                    -35                    -30                    -25  
 Cys Arg Asn Val Asn Gly Tyr Ser Tyr Lys Val Ala Val Ala Leu Ser  
                     -20                    -15                    -10  
 Leu Phe Leu Gly Trp Leu Gly Ala Asp Arg Phe  
                     -5                    1

## (2) INFORMATION FOR SEQ ID NO: 390:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Normal prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -19..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.6  
seq LLWLALACSPVHT/TL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro  
                     -15                    -10                    -5  
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Thr Ser Gly  
                     1                    5                    10

## (2) INFORMATION FOR SEQ ID NO: 391:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -42..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.6  
seq ASLFLLLSLTVFS/IV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu  
-40 -35 -30  
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu  
-25 -20 -15  
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala  
-10 -5 1 5  
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr  
10 15 20  
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe  
25 30 35  
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser  
40 45

## (2) INFORMATION FOR SEQ ID NO: 392:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Umbilical cord

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -18..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 8.5  
seq LVLGLVLPILWA/DR

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

Met Val Ala Pro Gly Leu Val Leu Gly Leu Val Leu Pro Leu Ile Leu  
-15 -10 -5  
Trp Ala Asp Arg Ser Ala Gly Ile Gly Phe Arg Phe Ala Ser Tyr Ile  
1 5 10

```

Asn Asn Asp Met Val Leu Gln Lys Glu Pro Ala Gly Ala Val Ile Trp
15 20 25 30
Gly Phe Gly Thr Pro Gly Ala Thr Val Thr Val Thr Leu Arg Gln Gly
 35 40 45
Gln Glu Thr Ile Met Lys Lys Val Thr Ser Val Lys Ala His Ser Asp
 50 55 60
Thr Trp Met Val Val Leu Asp Pro Met Lys Pro Gly Gly Xaa Phe Glu
 65 70 75
Val Met Ala Gln Gln Thr Leu Glu Lys Ile Asn Phe Thr Leu Arg Val
 80 85 90
His Asp Val Leu Phe Gly Asp Val Trp Leu Cys Ser Gly Gln Ser Asn
 95 100 105 110
Met Gln Met Thr Ala Arg Val Phe Arg Trp Arg His Val Xaa Gly Leu
 115 120 125
Leu

```

## (2) INFORMATION FOR SEQ ID NO: 393:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Ovary

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -21..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.5  
seq LLTIVGLILPTRG/QT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

```

Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile
-20 -15 -10
Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser
-5 1 5 10
Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp
 15 20 25
Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Thr Trp Pro
 30 35 40

```

Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly  
 45 50 55  
 Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr Pro Arg  
 60 65 70

## (2) INFORMATION FOR SEQ ID NO: 394:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8.3  
seq LALSSLLSLLLFA/GM

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

Met Arg Ile Ala Asn Arg Thr Arg Phe Ser Leu Pro Phe Leu Ala Arg  
 -45 -40 -35  
 Gly Ala Gly Trp Thr His Gly Arg Gly Met Met Val Val Gly Thr Gly  
 -30 -25 -20  
 Thr Ser Leu Ala Leu Ser Ser Leu Leu Ser Leu Leu Leu Phe Ala Gly  
 -15 -10 -5 1  
 Met Gln Met Tyr Ser Arg Gln Leu Ala Ser Thr Glu Trp Leu Thr Ile  
 5 10 15  
 Gln Gly Gly Leu Leu Gly Ser Gly Leu Phe Val Phe Ser Leu Thr Ala  
 20 25 30  
 Phe Asn Asn Leu Glu Asn Leu Val Phe Gly Lys Gly Phe Gln Ala Lys  
 35 40 45  
 Ile Phe Pro Glu Ile Leu Leu Cys Leu Leu Leu Ala Leu Phe Ala Ser  
 50 55 60 65  
 Gly Pro

## (2) INFORMATION FOR SEQ ID NO: 395:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -35..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.3  
seq NLLLLHCVSRSHS/QN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

Met Val Leu Gly Gly Cys Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln  
-35 -30 -25 -20

Ala Ala Leu Leu Leu Gly Asn Leu Leu Leu Leu His Cys Val Ser Arg  
-15 -10 -5

Ser His Ser Gln Asn Ala Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly  
1 5 10

Ala Ala Gln Pro Glu Gly Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly  
15 20 25

Asp Pro His Ser Pro Val Ile Leu Xaa Ser Tyr Leu Pro Asp Glu Phe  
30 35 40 45

Ile Glu Cys Glu Asp Arg  
50

(2) INFORMATION FOR SEQ ID NO: 396:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: AMINO ACID

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(D) DEVELOPMENTAL STAGE: Fetal

(F) TISSUE TYPE: brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -53..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix

(D) OTHER INFORMATION: score 8.1  
seq IYALFLLVGVCA/CV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys  
                   -50                                  -45                                  -40

Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly  
                   -35                                  -30                                  -25

Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val  
                   -20                                  -15                                  -10

Gly Val Cys Val Ala Cys Val Met Leu Ile Pro Gly Met Glu Glu Gln  
                   -5                                  1                                  5                                  10

Leu Asn Lys Ile Pro Gly Phe Cys Glu Asn Glu Lys Gly Val Val Pro  
                   15                                  20                                  25

Cys Asn Ile Leu Val Gly Tyr Lys Ala Val Tyr Arg Leu Cys Phe Gly  
                   30                                  35                                  40

Leu Ala Met Xaa Tyr Leu Leu Leu Ser Leu Leu Met Ile Lys Val Lys  
                   45                                  50                                  55

Ser Ser Ser Asp Pro Arg Ala Ala Val His Asn Gly Phe  
                   60                                  65                                  70

## (2) INFORMATION FOR SEQ ID NO: 397:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -57..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 8  
seq IVRLVAFCPFASS/QV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Val Leu Leu His Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu  
                   -55                                  -50                                  -45

Leu Ala Leu Lys Glu Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val  
                   -40                                  -35                                  -30

Glu Glu Ser Val Leu Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu  
                   -25                                  -20                                  -15                                  -10

Val Ala Phe Cys Pro Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala  
                   -5                                  1                                  5



```

Asn Ala Val Ser Glu Gly Val Val His Glu Asp Leu Arg Leu Leu Leu
 10 15 20
Glu Thr His Leu Pro Ser Lys Lys Lys Lys Val Leu Leu Gly Val Gly
 25 30 35
Asp Pro Lys Ile Gly Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys
 40 45 50 55
Gln Thr Gly Gly Val Ile Ala Glu Ile Leu Arg Xaa Val Arg Leu His
 60 65 70
Phe His Asn Leu Val Lys Gly Ser Asp Arg Cys Xaa Gln Leu Val Lys
 75 80 85
His Ser Trp Gly Trp Asp Thr Ala Ile Pro Met
 90 95

```

## (2) INFORMATION FOR SEQ ID NO: 398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Colon

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -47..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.9  
seq LLLPRVLLTMASG/SP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

```

Met Ser Gly Gly Arg Ala Pro Ala Val Leu Leu Gly Gly Val Ala Ser
 -45 -40 -35
Leu Leu Leu Ser Phe Val Trp Met Pro Ala Leu Leu Pro Val Ala Ser
 -30 -25 -20
Arg Leu Leu Leu Leu Pro Arg Val Leu Leu Thr Met Ala Ser Gly Ser
 -15 -10 -5 1
Pro Pro Thr Gln Pro Ser Pro Ala Ser Asp Ser Gly Ile Gly
 5 10 15

```

## (2) INFORMATION FOR SEQ ID NO: 399:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -26..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.8  
seq LVGFILFLTRSRG/RA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

```
Met Val Ala Pro Val Trp Tyr Leu Val Ala Ala Leu Leu Val Gly
-25 -20 -15

Phe Ile Leu Phe Leu Thr Arg Ser Arg Gly Arg Ala Ala Ser Ala Gly
-10 -5 1 5

Gln Glu Pro Leu His Asn Glu Glu Pro Gly
10 15
```

(2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLVRKLPLCHG/LP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

```
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
-45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
-30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
```



Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Ala  
           30                                  35                                  40  
 Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg  
           45                                  50                                  55  
 Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe  
           60                                  65                                  70                                  75  
 Leu Met Thr Cys

## (2) INFORMATION FOR SEQ ID NO: 402:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq LLMLLLFLSELQY/YL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr  
           -45                                  -40                                  -35  
 Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile  
           -30                                  -25                                  -20  
 Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr  
           -15                                  -10                                  -5  
 Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg  
           1                                  5                                  10                                  15  
 Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro  
           20                                  25                                  30  
 Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp Val Ala Gly Glu Gln Gln  
           35                                  40                                  45  
 Leu Asp Val Glu His Asn Leu Phe Lys Gln Arg Leu Asp Lys Asp Gly  
           50                                  55                                  60  
 Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu  
           65                                  70                                  75                                  80

Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro  
                   85                                  90

## (2) INFORMATION FOR SEQ ID NO: 403:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -48..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.6  
seq FLLVRKLPPLCHG/LP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

```

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 -45 -40 -35

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 -30 -25 -20

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 -15 -10 -5

Leu Pro Thr Gln Arg Glu Asp Gly Asn Xaa Cys Asp Phe Asp Trp Arg
 1 5 10 15

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 20 25 30

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 35 40 45

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 50 55 60

Gly Leu Leu Xaa Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 65 70 75 80

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa Tyr Phe Asn Asp Lys
 85 90 95

```

## (2) INFORMATION FOR SEQ ID NO: 404:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids

(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq PMLLRALAQAARA/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala  
                  -15                  -10                  -5  
Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val  
                  1                                  5                                  10  
Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met  
          15                                  20                                  25  
Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu  
          30                                  35                                  40                                  45  
Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Ala  
                  50                                  55                                  60  
Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg  
                  65                                  70                                  75  
Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile  
          80                                  85                                  90  
Ala Cys Lys Leu Cys  
          95

(2) INFORMATION FOR SEQ ID NO: 405:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Brain

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -19..-1

(C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.4  
 seq PMLLRALAQAARA/GP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```

Met Arg Cys Leu Thr Thr Pro Met Leu Leu Arg Ala Leu Ala Gln Ala
 -15 -10 -5

Ala Arg Ala Gly Pro Pro Gly Gly Arg Ser Leu His Ser Ser Ala Val
 1 5 10

Ala Ala Thr Tyr Lys Tyr Val Asn Met Gln Asp Pro Glu Met Asp Met
 15 20 25

Lys Ser Val Thr Asp Arg Ala Ala Arg Thr Leu Leu Trp Thr Glu Leu
 30 35 40 45

Phe Arg Gly Leu Gly Met Thr Leu Ser Tyr Leu Phe Arg Glu Pro Xaa
 50 55 60

Thr Ile Asn Tyr Pro Phe Glu Lys Gly Pro Leu Ser Pro Arg Phe Arg
 65 70 75

Gly Glu His Ala Leu Arg Arg Tyr Pro Ser Gly Glu Glu Arg Cys Ile
 80 85 90

Ala Cys Lys Leu Cys Glu Ala Ile Cys Pro Ala Gln Ala Ile Thr Ile
 95 100 105

Glu Ala Glu
110

```

## (2) INFORMATION FOR SEQ ID NO: 406:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Substantia nigra

## (ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -21..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 7.4  
 seq ILPLLFGCLGVFG/LF

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
 -20 -15 -10

```

```

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
-5 1 5 10
Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
15 20 25
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
30 35 40
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
45 50 55
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
60 65 70 75
Val Xaa Xaa Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
80 85 90
Glu Ile Cys Ser
95

```

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Lymph ganqlia

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide  
(B) LOCATION: -29..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 7.4  
seq LLLVTWVFPTVT/ET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Pro | Ala | Val | Phe | Leu | Ser | Leu | Pro | Asp | Leu | Arg | Cys | Ser | Leu |
|     |     |     |     | -25 |     |     |     |     | -20 |     |     |     |     | -15 |     |
| Leu | Leu | Leu | Val | Thr | Trp | Val | Phe | Thr | Pro | Val | Thr | Thr | Glu | Ile | Thr |
|     |     |     | -10 |     |     |     |     | -5  |     |     |     |     | 1   |     |     |
| Ser | Leu | Asp | Thr | Glu | Xaa | Ile | Asp | Glu | Ile | Leu | Asn | Asn | Ala | Leu |     |
|     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 63 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Brain

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -20..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.4  
seq LVFCVGLLTMAKA/ES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

Met Ala Ser Leu Gly His Ile Leu Val Phe Cys Val Gly Leu Leu Thr  
-20 -15 -10 -5

Met Ala Lys Ala Glu Ser Pro Lys Glu His Asp Pro Phe Thr Tyr Asp  
1 5 10

Tyr Gln Ser Leu Gln Ile Gly Gly Leu Val Ile Ala Gly Ile Leu Phe  
15 20 25

Ile Leu Gly Ile Leu Ile Val Leu Ser Arg Arg Cys Arg Phe Arg  
30 35 40

(2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Spleen

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -23..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.3  
seq ALSLLLVSGSLLP/GP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu  
-20 -15 -10

Val Ser Gly Ser Leu Leu Pro Gly Pro Gly Ala Ala Gln Asn Glu Pro

-5

1

5

Arg Ile Val Thr Ser Glu Glu Val Ile Ile Arg Asp Ser Pro Val Leu  
 10 15 20 25  
 Pro Val Thr Leu Gln Cys Asn Leu Thr Ser Ser Ser His Thr Leu Thr  
 30 35 40  
 Tyr Ser Tyr Trp Thr Lys Asn Gly Val Glu Leu Ser Ala Thr Arg Lys  
 45 50 55  
 Asn Ala Ser Asn Met Glu Tyr Arg Ile Asn Lys Pro Arg Ala Glu Asp  
 60 65 70  
 Ser Gly Glu Tyr His Cys Val Tyr His Phe Val Ser Ala Pro Lys Ala  
 75 80 85  
 Asn Ala Thr Ile Glu Val Lys Ala Ala Pro Asp Ile Thr Gly His Lys  
 90 95 100 105  
 Arg Ser Xaa Asn Lys Asn Glu Gly Gln Asp  
 110 115

## (2) INFORMATION FOR SEQ ID NO: 410:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -36..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.2  
seq IMLLSLAAFSVIS/VV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Ala Val His Asp Leu Ile Phe Trp Arg Asp Val Lys Lys Thr Gly  
 -35 -30 -25  
 Phe Val Phe Gly Thr Thr Leu Ile Met Leu Leu Ser Leu Ala Ala Phe  
 -20 -15 -10 -5  
 Ser Val Ile Ser Val Val Ser Tyr Leu Ile Leu Ala Leu Leu Ser Val  
 1 5 10  
 Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val Ile Gln Ala Val Gln Lys  
 15 20 25  
 Ser Glu Glu Gly His Pro Phe Lys Ala Tyr Leu Asp Val Asp Ile Thr

30

35

40

Leu Ser Ser Glu Ala Phe His Asn Tyr Met Asn Ala Ala Met Val His  
45 50 55 60

## (2) INFORMATION FOR SEQ ID NO: 411:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymph ganglia

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLWTLLLFAPFG/LL

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Xaa Gly Ser Val Glu Cys Thr Xaa Gly Trp Gly His Cys Ala Pro  
-30 -25 -20

Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly  
-15 -10 -5

Leu Leu Gly Glu Lys Thr Arg Gln Val Ser Leu Glu Val Ile Pro Asn  
1 5 10 15

Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Ala Val Gly Thr  
20 25 30

Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val  
35 40 45

Val Met Val Ala Thr Asn Thr Pro Pro Gly  
50 55

## (2) INFORMATION FOR SEQ ID NO: 412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Normal prostate

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -29..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LIFLCGAALLAVG/IW

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu  
                  -25                  -20                  -15  
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val  
                  -10                  -5                          1  
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser  
          5                          10                          15  
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly  
          20                          25                          30                          35  
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Xaa Gly Ala Lys Xaa  
                  40                          45                          50  
Glu Xaa Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile  
                  55                          60                          65  
Phe

(2) INFORMATION FOR SEQ ID NO: 413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Testis

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -32..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7.1  
seq LLWTLLLFAAPFG/LL

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Met Arg Gly Ser Val Glu Cys Thr Trp Gly Xaa Gly His Cys Ala Pro  
          -30                  -25                          -20  
Ser Pro Leu Leu Leu Trp Thr Leu Leu Leu Phe Ala Ala Pro Phe Gly

-15                      -10                      -5  
 Leu Leu Gly Glu Lys Thr His Gln Val Ser Leu Glu Val Ile Pro Asn  
   1                      5                      10                      15  
 Trp Leu Gly Pro Leu Gln Asn Leu Leu His Ile Arg Xaa Val Gly Thr  
                     20                      25                      30  
 Asn Ser Thr Leu His Tyr Val Trp Ser Ser Leu Gly Pro Leu Ala Val  
                     35                      40                      45  
 Val Met Val Ala Thr Asn Thr Pro His Ser Thr Leu Ser Val Asn Trp  
                     50                      55                      60  
 Ser Leu Leu Leu Ser Pro Glu Pro Asp Gly Gly Leu Met Val Leu Pro  
   65                      70                      75                      80  
 Lys Asp Ser Ile Gln Phe Ser Ser  
                     85

## (2) INFORMATION FOR SEQ ID NO: 414:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Lymphocytes

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -15..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq LRLCLKLAATSASA/RV

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Ala Leu Arg Leu Leu Lys Leu Ala Ala Thr Ser Ala Ser Ala Arg  
 -15                      -10                      -5                      1  
 Val Val Ala Ala Gly Ala Gln Arg Val Arg Gly Ile His Ser Ser Val  
                     5                      10                      15  
 Gln Cys Lys Leu Arg Tyr Gly Met Trp His Phe Leu Leu Gly Asp Lys  
                     20                      25                      30  
 Ala Ser Lys Arg Leu Thr Glu Arg Ser Arg Val Ile Thr Val Asp Gly  
                     35                      40                      45  
 Asn Met  
   50

## (2) INFORMATION FOR SEQ ID NO: 415:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (F) TISSUE TYPE: Cancerous prostate

## (ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: -65..-1
- (C) IDENTIFICATION METHOD: Von Heijne matrix
- (D) OTHER INFORMATION: score 7  
seq IGHFLCLVILVYC/AE

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

```

Met Pro Ser Ala Phe Ser Val Ser Ser Phe Pro Val Ser Ile Pro Ala
-65 -60 -55 -50

Val Leu Thr Gln Thr Asp Trp Thr Glu Pro Trp Leu Met Gly Leu Ala
 -45 -40 -35

Thr Phe His Ala Leu Cys Val Leu Leu Thr Cys Leu Ser Ser Arg Ser
 -30 -25 -20

Tyr Arg Leu Gln Ile Gly His Phe Leu Cys Leu Val Ile Leu Val Tyr
 -15 -10 -5

Cys Ala Glu Tyr Ile Asn Glu Ala Ala Ala Met Asn Trp Arg Leu Phe
 1 5 10 15

Ser Lys Tyr Gln Tyr Phe Asp Ser Arg Gly Met Phe Ile Ser Ile Val
 20 25 30

Phe Ser Ala Pro Leu Leu Val Asn Ala Met Ile Ile Val Val Met Trp
 35 40 45

Val Trp Lys Thr
 50

```

## (2) INFORMATION FOR SEQ ID NO: 416:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: AMINO ACID
- (D) TOPOLOGY: LINEAR

## (ii) MOLECULE TYPE: PROTEIN

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(F) TISSUE TYPE: Testis

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: -154..-1  
(C) IDENTIFICATION METHOD: Von Heijne matrix  
(D) OTHER INFORMATION: score 6.7  
seq ALGILVVAGCSFA/IR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

Met Ala Leu Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile  
                  -150                  -145                  -140

Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Xaa Asp Gly Tyr  
                  -135                  -130                  -125

Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser  
                  -120                  -115                  -110

Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg  
                  -105                  -100                  -95

Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu  
                  -90                  -85                  -80                  -75

Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala  
                  -70                  -65                  -60

Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn  
                  -55                  -50                  -45

Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys  
                  -40                  -35                  -30

Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly  
                  -25                  -20                  -15

Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys  
                  -10                  -5                  1                  5

Lys Ala Thr

(2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids  
(B) TYPE: AMINO ACID  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
(F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide

(B) LOCATION: -70..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.7  
 seq LAFSLPALPLAEL/QP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

```

Met Ala Ala Ser Thr Ser Met Val Pro Val Ala Val Thr Ala Ala Val
-70 -65 -60 -55

Ala Pro Val Leu Ser Ile Asn Ser Asp Phe Ser Asp Leu Arg Glu Ile
 -50 -45 -40

Lys Lys Gln Leu Leu Leu Ile Ala Gly Leu Thr Arg Glu Arg Gly Leu
 -35 -30 -25

Leu His Ser Ser Lys Trp Ser Ala Glu Leu Ala Phe Ser Leu Pro Ala
 -20 -15 -10

Leu Pro Leu Ala Glu Leu Gln Pro Pro Pro Pro Ile Thr Glu Glu Asp
-5 1 5 10

Ala Gln Asp Met Asp Ala Tyr Thr Leu Ala Lys Ala Tyr Phe Asp Val
 15 20 25

Lys Glu Tyr Asp Arg Ala Ala His Phe Leu His Gly Cys Asn Ala Arg
 30 35 40

Xaa Ala Tyr Phe Leu Tyr Met Tyr Ser Arg Tyr Leu Ser
45 50 55

```

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids  
 (B) TYPE: AMINO ACID  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens  
 (F) TISSUE TYPE: Hypertrophic prostate

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
 (B) LOCATION: -24..-1  
 (C) IDENTIFICATION METHOD: Von Heijne matrix  
 (D) OTHER INFORMATION: score 6.6  
 seq KMVHLLVLSGAWG/MQ

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

```

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
-20 -15 -10

Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val

```